

1 AACCCATGTT AGTGTGCAGT TCTGCTGGCA CACACATGCA GTTGTGTAAC
51 CACTACCACC AAAAGCAAGA TGTAAAATAG CTCCATCACC CCCACAAGCC
101 TTCTGATGCT CTTTGTGCAT CAATTCCCTT CCCGCTAGTC ACAACTGGTA
151 ACTACTGATT TGTTTTCTGT CCCTATAGTT TTGCCTTTTC CAGAATGTCA
201 TTGTTGACAG GTATCAGTAA TTCATTCTT TTTATTGCTA ATTACTATCT
251 CACTGTATGA ATGCAACACA GGTGTTTAC CAGTTCACCC GTTAAAGAAC
301 ATTTTGTTC TGCGCTTGAC AGTTATGAAT AGAACTGCTA TAAACCCTCA
351 AGTAAAAGTT TTGGTGTGAA GATAATTTTC TCAGCAAAAA CGCTGACAGG
401 TAATTTTCT AAGTATTACT TTTTAAAAA AGTAAAATAG CCTGTAGCCC
451 CAGCTACTCA GGAGGCTGAG GCAGGAGAAT AGCTTGAACC CAGGAGGCGG
501 AGGTTGCAGT GAGTTGAGAT TGTGCCACTG CATTCCAGCC TGGGCGACAG
551 AGCTAGACTG TCTCAAAGAA AAAAAAAAAA AATAACAAAT AAATAAAAAG
601 TAAAATGAAA GCATGTAAGT GTAAGATGAC TAGTTCAAGC AACCTCTCTT
651 CAAGTACAGA GTATTACAGAG TAGAGATTAA AAGAGGTTTT CAAGGACAGA
701 GAAAATTTGA AGTTTGAAGG CAGTTCCAAA GGAAGGCAAT GATTCTTAAT
751 AAGACTGGAA GTTGAAGTA ATATAAAAAG ATAAATCAGT TTCAAGATGA
801 TTTTACTAAG CAGGCAGCCC TTAATTTACA AATTCTAGAT TCATACATAT
851 CTTAAACATA CAAAATGATA TGAGGAGAGG TAAGTTCAGG GTCTGAGTTC
901 CTGGCTGTTG TTGGAAGTGA TTTCTGTGTA GTGATTCAGA AGATGTGAGA
951 CACCCTAATT TACAAGTACA GAGGTATCTT CTTTTCTGCA AACAGCAGTA
1001 CAACAATAGT TCCTCTTACG CAGCTGTGAA TGAACAGGAT TATTACAATT
1051 AATGATATCT CATTTGATTG GCGCCTTAGA GAATTAAGAC CTTTCACACC
1101 TAATATACAA CTTTGTGTG AAGGCAGATA TTTATATTCT CATTTTACTG
1151 ATGAGAGACT ACCCGGAGAC GCTATGTCAC ACCTGAAGGA TTAGGTACTT
1201 TCTCTGTTAA GTCCAATGTT CCTTCCGTTA TTCCATGCTA GGCAGTAATA
1251 AGTTCGTGCT TGCCTGAGTA ATAAGCTCCA AACCTCGGAA CTGCACCCAT
1301 CTTGAGAAGG AGGAGGGCGC TGTGGTTTTT TCTGATAAGT GCAGCTGGCA
1351 GACACTCTAT ACGCTTAATC ACGGGCAAAT CCTACCTAAG CTGCCTACCA
1401 AACTAGTCTT TCTTTTCCCC GTTGCCACG CAGATGGCTG TTGATCTTTT
1451 CTGCAACAAA TCCAGGAGTT TCTCCTTTT GTTTTATAAT TGCTCCAATA
1501 GATGCTTTAG GATTAACTC TCTGCTTTT AAAGCAGAAT CGCCATCCCA
1551 GGTGTGCAAC CACGAAAAAA TTAGACATCC GTGAGAGACA ATGCCCTCCA
1601 TGGCCCAAGT TCCAGGCAGA GAGAAGCAGC TCTGGGCTGA CCGCCAAGGC
1651 TCCGGCCCGA GAGGGTCTTT AAGTGGAGTA ACCAGTCTTC AAGACCCCGC
1701 TCCCAAGCCA CCGACGCGCT GACGCTGCAG CCCTGGACCT GCTGGGGGCC
1751 TCTTCCTCGG ACCCGCATGC TGACAGCGGG ACTGGCAACT GGGCAGAGGT
1801 CGACCCCGGG TCCGCACAGC ACCTCCCGAG ACCCAGCTCC CAGCTCCCTC
1851 ACTTCGGCT CTCTGGAGGC GGGCCCGGCC AGTGCCGCG AGGCCAGCGC
1901 GCGGAGCTCC TCCCCAGCAG CGGCGGGACG GCCACACCT GCGCGCCGCG
1951 CGGGCTCGGG TGGGGTCTCC GCTCCTGCGC CTGCGCGCC GCAGCCGCAC
2001 CCCCACGGC GCCCAAACG CTGTTGCGCC GCGCGCCCG CCCAGCCCGG
2051 CCTCGCGCT GTCCCGTCT CGCCCGCAG CCTCGATCT CCCGTGACTT
2101 CCTCGGCCAG GCCCCTGCG CCTCTGGGAC CATGTTGCGC TGGCTGCGGG
2151 ACTTCGTGCT GCCCACC GCGCCTGCCAGG ACGCGGAGCA GCCGACGCGC
2201 TACGAGACCC TCTTCAGGC ACTGGACCGC AATGGGGACG GAGTGGTGGA
2251 CATCGGCGAG CTGCAGGAGG GGCTCAGGAA CCTGGGCATC CCTCTGGGCC
2301 AGGACGCCGA GGAGGTGGGT CGCCGCCGGG GCGCCGCTG AGCGTAGGGA
2351 GGGCTGCGGG CGCTGGGGAC ACTGCGAGGA CCGAGGAGGG CGGCGGCTTG
2401 AGGCGTTGCC AGGAGAGGAA GGAGGAACTG TGGCGCCAG CGCTCCGGTG
2451 GCTTCAGAAA CTCGGGCGTG GGGCCGCGAC CGGCGACCCC GGTAACAGAA
2501 GTGGGTCATA ATACGAAAGT CTAAGTGGTAT TTGTCCAGAT AAAATGAGTG
2551 TTGTGGACAC TCTGGCCAC GGGCACTGTT AAATTTTAA GAACTTTTG
2601 TCCTGAATCC ATCCCAGGTT CTTTGTTTT TGTTTTAAATA CCTTGCAGAC
2651 ATGTAATCCG TTTTAGCTGT CAGACTTCAG TGGGTCCCAA GTTTTGTATA
2701 AAGGCGCACA TACTCGATCT CTTTCGAAGC TGCTTTGTTA CAGCAGCTAT
2751 GTGTATTGTC TACTGTTTGA AAAGTGTGTT AAAACCAATC GCGTGTGTTCC
2801 CCCACTTCCT GTTGAGAAGG AATGGCGGCA TTCCATTGTT TAAGACATTC
2851 CTAGGTTAAT GCCCTAGGTA CATAAATTGA TCTGAAGGGT TGACTTGACC

FIGURE 3-1

2901 TGCGACTGAG CAATTTTCATT TTCTCTGAGT CATCTTAACT GTGCCCCCTGA
 2951 ACTTCTGCCC CTTTAGTAGG GTGGAGATAT GTGGAACCTC TCCAACCCTG
 3001 TTGAAGCGTT CCCTGACACT GGCATTCTCT TATCCAAAAG GGGAAAGTGA
 3051 TTAGGTTACT ATGAGGGCCA ACAACTGTTA TATAGTTATA TTTCACTTCT
 3101 CTTTTAATGT CTTTGGTAGT TATAGGCCTC TTCAGTTTAC TGTTTCTTCT
 3151 AGAGTCAGAT TTAGTAAGTT ACAATTTTTT TTGAACTGC CTGTTCTGTC
 3201 CAAGGTTTCAT AATACTCACC GATGATTTTA TAACACTTCT GACTGAATCT
 3251 GTAGGTAGGT TCTCTATTTT ATTCTCATA TCTATCCTTT TCTCCCCCTC
 3301 AATCTTGCCA AAGTTTTGTG TATTTTATTC ATACTTTGAA GGAACCAACT
 3351 TTTGGTACTT TGTGCTGATT GTCCCAGAAA TGGCCAGTT GGAGTTCCCC
 3401 ACCATGTCCA ATCATTGGCT GGAAGCAGCC CAGGAAAGGG ACGACCTTGC
 3451 TGCAGTGCAT CAGCAGATGC CAGGGTTAGA GGCTAGAGAG TGGAAGTCAA
 3501 CTGTGTTCTT CACAGTAGGT GCCTTTGAAG GGAGATCTCA GTGGTACAAC
 3551 TCCATGGTCC CTACAATATA CAAAAGCTCT TTGGAGTGCT CAATGATTTT
 3601 TAAGATTGTA AAGGGATCCT GAGATCAAAA AGCTTGAGAA TTGCTGCTGT
 3651 ATCACCATT TACGTAAC GCATCATATT CTGTTATATG TTTGTGTCAT
 3701 AGTATATGTT ACCAATTCCT TTTAAATCAC CTTTTACTTT ATTGATAGTT
 3751 TAAAAACGAT TGTAAAGTGA ATTGCAATGG ATGTCCTTTG TATTCATTTT
 3801 CTCATTCTGG TCCAGTTACT TTCGTAGGAT AAATTTTGAG GAGTGGACAT
 3851 TGCTGAGTCT GAAGGTAACA CACATTTTAA ACTGGGATAC GTATTGCCTT
 3901 TCGGAAACCT TAGACCCATT TTCACTCTTT TGA CTGACAG TGCTTGCTTC
 3951 TCCACATCCT CGCTCATTCA GGGTATCAGT CTTTGTAAAG TCTCCTATTC
 4001 TGCAGGTGAA ATTCTTTTTC ATTTCTGTCT TTAGTCCATT TAGTGTGCT
 4051 ATAGTGAAT ATCTGAGACA GGGTAATTTA TAAAGAAAAG ACATTTATTT
 4101 AGCTCACAGT TCCGCAGGCT GGGAAAGTTA AGAAGCGTGG TGCTGGCATC
 4151 TGCTGGACTC CTGGGGAGGG CTTTCTGCT GTGTCACAAC ATGGTGGAAA
 4201 GTCAAAGTGG AAGTGGACAT GTGTGAAGAA GCAAAATCCG AGGGGTGTCC
 4251 TGGCTTTATA GCAACCCAGC CTCGAGGGAA CTGATCCATT ACTGAGGGAA
 4301 CTAATTCAGT CTCATGAGAG AGAGAACTCA CTCACTACTG CAAGAATGAC
 4351 ACCAAGCCAT TCATGAGGGA TCTGCCTCCG TAACCCTGAC ACCTCCTGCT
 4401 AGGTCCCTCC TCCCAACACG GCCACATCAG GGATCAGACT TCAACATGAG
 4451 TTTTTGTGGG GACAAACAAA ACGTAGCACT TGCTTTGCCT TTTGGTTCTA
 4501 TTCACATCCT CCACAGGATT GCATTATGCC TACCCATTTG GTGAGGGCAG
 4551 TCTTCTTTAA TTGGTTTACT GATTCAAATG CTACCTCCT CCAGAGACAT
 4601 CCTCACAGAC ACACCCAGAA ATCATGTTTT ACCAGTTATC TGGGCATCCC
 4651 TTAGTCCAGA CGAGTTGATA CATAAAATTA ACCATCACAC ATGGGATAGA
 4701 ATTAGGATTA CACAGTCAAC CTTTATGGGA GAAAATTTCA GAGGCATGTC
 4751 AGGGGTTTAT GTAATGTCAA GGAGTGAGGA CATTGGCTAC TTGAGCATAG
 4801 AAATGAGAAC TGTGGGGTGA CTCTTCGGTG GAAAGTTTCA AGGTAGTAGT
 4851 TTGTATCTAA GCCAAATACT CAGCTTGAAG CAAAATCTCT ATAAATTTTC
 4901 ATCTGATTTG ATCTCATCTC CGTGTTTCCA AGCATTTGTA ATGAATTGAG
 4951 CATTTAGAAG AGAACAATT TCTGTTTAAG TTTCTTTAGA TTTTAGATGG
 5001 AAAGAATGTA GAAATAAGAG TAGAATGTAG AAATAGGTAT AAAGAATATA
 5051 ATAGCTAACC ATTACTAAGT GTTCCAGAAT TATCCAGGGA AGAGAAAAGA
 5101 ATTCAAGGCA AGTCCTGAGA CAAAATTAAG AACCAATTGG AAGTGAAAGC
 5151 GCTACATTTT TTTTTTCTGG TATGACCTTT CTTTCTATA TGTTCCAAAT
 5201 CTCCTCACTA TGAAATTAGT GAAAAATTAA AGTTAAAAAT TAGAGAAAAT
 5251 TCACATTAAG TTCTCCTAGG ACTCAGTAGT ATAAGGGTAT AGACTGAGAG
 5301 TAGAATGTAG TGTGAGAACA AGGAGATACA GTATTTAACC ATTACTAATT
 5351 CTCTTATACT TGTCTAGTAA TCCTATTTCC TTTTAAAAGT CTTCAATTAT
 5401 TTTCTCTTTA CGCACCTCCT TCTCCCTCTT GTCTTCTCCT TTCTACCCCC
 5451 ATCTTTCTTC CTGTGGAGCC TTCATGAATG GGATTAGTGC TTGTATAAAA
 5501 GTGACCTGGA AGACCTTCCT TGCCCTTCC ACCATGTGAG GACACAGTGA
 5551 GAAAACAGTG GTCCATGGAA CCGGAAAGTG GGTCTCACT AGACAGTAAA
 5601 TCTCCTAGCA TTCGATCTA GGACTTCCAG TGTCTGGAAC TGCAAGAAAT
 5651 CAATGCTTAT TGTTTAAGTA AGCCAGTAGT ATTTTGTGCA TAGCAGCCCA
 5701 GTTGGACTAG GACAATTACC AAGAGCAAGA AGGGAAGCAG CAAGCTACAA
 5751 GAGAGTCCG TCCTTGGTGT AAATTGACCG TGTAATCCTT GTCAAGTTTG

FIGURE 3-2

5801 AGCCTTACTG GAGCTTTACT TTCTTATTCT TAAAATGCAG ATATCTTGCC
5851 TGCATCCTGG ACAGAGCTTT TAACAAGGTC ATATGTTGCA GAATATGAAA
5901 GTTCATGTTA AAAAACCTTT TAAAATGTGG TATCCCATTT ACTAGCTGGT
5951 GAACTTCTTG AGGAACCTCT GTGCCCATGG GTATGAAGTG TATGCTGAAT
6001 GATCACCCAA TGTTAGAGGA GTGGGTGGAC TGGTAACCTG ATTTAAGGGC
6051 CATTCTAACT CTTACATTCT ATGATTTTTT TAATTCTGTC TTTAAGTTTT
6101 TACATTTACA ATCACAGAAA AAATAGTCAC ATAGAAGAAT AGTAGCTTAG
6151 CAAATGTTTA TTGCATTGAG TGGAAATCAGG ATTTCACTCC ATTAAGTAAT
6201 TCCTCTGTTA ACAAAGAGGG TTCATTTTCAT TTTTATTTCA TTAATATTGC
6251 TTTTTTTTTT TTTTTTCTGG AGACAGAATC TTGCTCTATC ACCAAGGCTG
6301 GAGTGCAGTG GTGCGATCTC GGCTCACTGC AGCCTCTGCT TCCTGGATTCT
6351 AAGCGATTCT TGTGCCTCAG CCTCCCAAGC AGCTGAGATT ACAGGCACAT
6401 GCCACCACAC CTGGTTAACT TTTGTATTTT CTAGTAGAGA TGGGATTTTG
6451 CCATGTTGGT CAGGCTGGTC TTGAATTCCT GGCCTCTAGT GATCTGCCTG
6501 CCTCTGCCTC TGAAAGTGCT AAGATTACAG GCATGAGCTA CCATGGCCAG
6551 CCCATTTCTT TAATATTTTA ATTGTCAGAC ATGTTATGGT TTCTGGCACA
6601 ATATTAAGAA GACATGATAT GAAATCACAG GGTGAATTTT AGGGCATCAC
6651 AACAGAAAGA TTATGGTATA AGAAAAACAA TGGAATTCCA ACTACATTTT
6701 TGTCAAATGT TCTAAAATAT ATAAAATCTG TATCTTTTGT GTTCTCTCCT
6751 GATTTATATT CTAAATTTGA TGTTATCCTT CTCTGCAGAA ATAAAGTGTC
6801 TGAAAGAATG AAAAAAATGG AAGAATTCTT TAGTAAGGTA TAAAAATCCC
6851 TTTCTATCTT TGTAGCATTCT TAAGCCTTTT GTCACCTTTC CAAACTCCCA
6901 ACATGCCATA TTCCCTGACT AGGCCACAGC CATGTACATT GATCCCTTTA
6951 TTTTCTTCTC TCTGCCTGAG ATTTCTCTCA TTCCCCCTTC TCTGCCTGGT
7001 ATATGATTGC CCATTGTTTA AGGCCCAAC TCACCTTTAT AATCTTCCTA
7051 GCCCACTTTC TTTATCGGTA TTCCAGAAAA AACAAAAGAA GCTTCCACAA
7101 GACAACATTC TGTAATACAC TGCTTAACTT CTTTGGACCC TGCTGAGTTC
7151 AAAAATCTTA TCTTTTTAAG GATTGAATGG AGTCCACCAA GGTATCTATA
7201 TTTGACAGGA TTTATGAAAA CAAAAGGATT TGTTGAGAAA GTTTGAAGCC
7251 TAACCTTGAA ACGTGGATCA TAGTGTTTAC TACACATTAA CTGTTTTAGT
7301 GGATGTAATA GTTATTATTA TAGGCTGTGG AATCAGAACA GGGTTCAAAT
7351 GTTTTCACCG CTTGCTAGAC TGTGGCCTTG GGCATGTTAT TTAATGCCTG
7401 GAGGCCTCAA ATGTTAACTA GGAATGGTAA GACCTACCCA GTAACCTAGC
7451 ATAAATAGTA AATTCATTCA TTTAATGTTT TCAAACAGTG CCAGACATTG
7501 TTTAATGAAC TGGGGATATA GTGGTGAACA ACACTGACAG CGTTCTTCAT
7551 TGTATTCTCA AAACCCTCCC TATAGTAAGT AGGTCTGTGT GTGTGTGTAG
7601 GTGCATGGGG AATAAAAAAT AATAAGCAAA TAATGAACAG GGTAAATTTCA
7651 AAAAGCAGAA AGAGCTATTCT AACAAAACTA CCTGCCTTTT ATTAGATGAA
7701 ACTCTCAACT CTATGGTTTG TTCTCTCCTG TCAATTCTGT TAAATGCTGT
7751 CAGCCTGTTT TCCTTATCAC CCTGGCCACG ACTTCTGTCT TTTCTGCTTG
7801 GTCCTGTAGA CTCTAACCCA AGGCTCATTCT TCTGCCTGGC TATCTGCCTT
7851 CTGTGGCTCT TTGCCACTAC CTACATTTTC TGTGTTGCAC AGGGAAGGAC
7901 CATTCCCTGT GGACCATAAA ATTCTCTTTT TGAAAGAATT CATTCTTGAT
7951 TGGGCCACAG CACATCTTGT GAAACAGCAT TAGACATTTG CCACTGCTCA
8001 GCAGCTCTGG GGGAAAATGT TTAAGTGAAG GCGTACAGTA GTTTTTTTGA
8051 CTAACCATGG TGCAACCTCC TCCCAGAGGG AAACCTATGA GTATTTCAAG
8101 GACATGTGAT GGTCTGTTTT TGTCCCCAGT ATCTGACATG ATGGGTAGTG
8151 TAGAGCAAGA GCTTACAGAT AATGGCTAAA TTAAATTTTC TTTTTGAATT
8201 TTAATATTCA ACTTTTTAGG GTACCCCAATC TCCATATTTA GGAAAAATAAA
8251 TTACATAAAA AGTGAGAGT TTTTATTGTG AAACCTGCACC TCCATATTCC
8301 CAGTGGTGCA GGATGAGGGA GCACAGGTGT TGGTCTGGGG AAGCCAGGGC
8351 CCTCTGTGGT TCTGGAGGGT GAGGATTAAG AGGAAGCCTT AGATAGTATT
8401 TATGAGTATC TGCTGACTTC TCTCTGGGAC CCAAGATCAC TGAACCTTTG
8451 CCTATTTTGA GATCATTTT CCAATCCAGC CACTAACAGC TGAAGGATAG
8501 GCTTGCCCTG GAGCCATTGT AGTGGTTTGA TGAAGATAAA AGATAAAAAA
8551 CTGTGAGGGG AGGTGTCACA GAAGAAAGGG CCCATGTGGG CAGATTTTCA
8601 TTCAATTCCT AGTCTTTATT ACAGCAATTC TCCAGTGCTG CAACCTTAGA
8651 AAAGGATTCC TACAACACAA TGTAGGTACC CATCAGCAGC AGATTGGATA

FIGURE 3-3

8701 AAGAAAATGT GGTACATACA CACCATGGAA TACTATGCAG CCATAAAAAA
8751 GGAGCAAAAT CATGTCCTTT GCAGCAATAT GAATGCAGCT GGAAGCCAAT
8801 AACTTAAACG AATTATTGTA GAAACAGAAA AACAAATACT GTGTTCTCAT
8851 TTACAGGGGG AGCTAAACCT TGGGTAAATG GGGCATAAAG ATGGGAACAA
8901 TAGACACTAG GGACTCCAAA AGGGGGGAGG GAGGGAGGAG GGCAAGGGCT
8951 GGAAAGCTTC CTA CTGTTGTTTAC AACCTGGGTG ATGGCAGCAT
9001 TAGGAGCTCA AACCCAGTA TCACACAGTA TACCCTTGTA ACAAGCTGAT
9051 GGTGTAACCC CTGAATCTAC AATAAAATTA TTTTATTTTA AAAAATCATT
9101 ATAAGGATTT TTA AAAAAGAA GGATTCTTAG ACAGGTGCAG CCAAACAATT
9151 TTTTTTAAAT GTTGGCAGGC CGCCACCGCC AGTCACTTAT GCTGCAATAG
9201 CCCATGTCCC AACATTCCCA ACCTACTTCT CTCCAAAAGA GAAGCTATAC
9251 TTTCAGATGG CCCTGTGCTG GGTCTCCCT GGAAGTTTCT GGGGAAAGGG
9301 GCTTGAGTTG CCCCAGACTG ACTCTTCCTG GAGTGGGAGC CGGGGCTTCT
9351 GATCAGACGT GAGTGAGGCA GGAACCTCCG GGTCTCCAG CGCAGCCCAG
9401 AGTGCGGTCC CACGAGGTC CCGGTCTCTG CGCGCTCGCG CCTTTGCGCT
9451 GAAGCCGTTA GGATGAGCCC TCTCCTTCCA GAGCTTTAAC CGATGAAGGT
9501 GCATTGTGTT TGGCGCCCCT GAGGAGGATG CTGTCTTAGG CCTCTTCCCA
9551 CTGGACGTGT GTGGTGGGCA GAGATCCCGT TCGTCGGTCG CACTTCCACC
9601 CCGCTGGGGC TCACTCAGGC CGCGGAGCTG CGAGGGAGAC ATCCTCGATG
9651 GACTCCCTCT ACGGAGATCT CTTTTGGTAC CTGGAATAA ACAAGGATGG
9701 GACCTTGGAC ATTTTGTAGC TTCAGGAAGG CCTGGAGGAT GTAGGGGCCA
9751 TTCAATCTCT AGAGGAAGCG AAGGTGGGTC TCACTGGGGC TGTAATCAGA
9801 GAGACGTTGG GGCTGGGAGC CCTGGAGAGG CATTGGGCAG AGAGGGCAAA
9851 ATTTACATGT TGTCAAGCTT GACCTGGGCC CACTGCAGTG TTCAGGTGGT
9901 TGACCAGCGT TACCGTTTAT TAAGAAATAAC AACACAGCTA ACACATTTCT
9951 CAAGTATTTT TCTCCGTTTT CTCCTTGCT GTAGTAAAAT CTCCAACCTC
10001 AGATTGCTCT CAAGATGTTG GCTACATACA GCCTTGCTT AGGAGTCACC
10051 TTGTTCAATG TGCTCACCTG TCATTAGTCA CCCAGAGGGG CGTCTAGGCT
10101 AAAGATGCGC CCTCCCCAGT TCAGAGAACT GGAATAATCA CTCTACGTGT
10151 ATTTGGGTGA GGGGTGGTGA TTGGAAATTT TCTGATGTTA TGTTTTGGTT
10201 TCTGTTCTCG GTGAAGGTGG CTTTTACTCT CGGGTTTCAC
10251 TAGTGCTGAG GTTTCCTCAT AATATGCCTT AATTGATAGA CCCTAGTTAT
10301 CAGTACCGAG CTTAGGCTAA CCCTTCTCTT CCCCAGAAGG CTAACCTACA
10351 GGCTCCTTCT CAGCATGTTG TGCTTCGTAC ATACTCCTAT TGCAGTATTT
10401 CCAAGTCATT TTTCATTTGG AATTTATTAT TGTATATAAT AATTACTTTA
10451 TAAGTATATT TGCTCTTTGG ATGTTTGACC CGGTAGACTG GGAGATCATG
10501 AGCATGTGGA CTATTGAGTT TATTTTGGAT AATTGGTACT TCGTGCCCAA
10551 AAAACTGTCA GTTGAGTTCT GTCATGTTGA AATTTAGTAA AACTCTTTCT
10601 ATTAGCCATG TGAACCTTGG GAATATTGAA GCATCCATTC AGTCATGGGT
10651 CAGTTCTAGT TTGAGCACAT TCTATATTCC AAGCCCCATA CCCTGGTATC
10701 CTCATCTGTT ATATCAGAGG CCTGGACTGT GTACTTTCTG TGGACCAATT
10751 CAGTCCAAAA TGTTATTTCT GCAAAGCTTA TCTGGATTTT TAATTCCTAG
10801 AAAAAAGCAG TGTTTCTCCT TTTAAAGTTA AGTGTTCTTG TTCAGGTGCA
10851 GTGGCTCATG CCTGTAATTC CAGCACTTTG GGAGGCCAAG GCAGGTGGAT
10901 CACTTGGGGT CAGGAGTTCA AGACCAGCCT GGCCAATATG GTAAAACCCC
10951 ATCTCTACTA AAAATGCAAA AATTAACCGG GTGTGGTGGT GGGTGTGTGT
11001 AGTCCCAGGA GGCTGAGGCA GGAGAATCAC TTGAGCCTGG GAGGCAGAGG
11051 TTGCAGCAAG CTGAGATTGC ATCACTGCAC TCCAACCTGG GTGACAGAGT
11101 GAGACTCCAT CTCAAAAAGA AAAAAAAAAA GTTAAGTGTT CTTCATATTT
11151 GTTTAAAGAC ACTCTTATAT TTAGATTTGC AAGTGTAAGT TGTATTTGTT
11201 TATTTGATAC AAAGTAGCCT TTCATAAGAA ATTCTGGGTT AGCTATCAAG
11251 TCGAATCTTT TGAAACACAT TTCTTCCTTA TTGAAACAAA AGGTTTGTAG
11301 AGCTGTCTTG CATTTTGGC AAGGACGCTT TGTGTACCTA GTGGTGACTG
11351 AGGAGGGTTC ACATGTCAAA ACCCAAGGGA GGGGTGTCCC CAGAGAATTC
11401 TTGACCAACC ACACAGAACA TTCTGTTTCA GAGGAGACC ATTGTGACTT
11451 TTCCTCAAGT GGCAGTCACA TCGTTAGGAG GTTTTGATGT GAGGTCTCTT
11501 CCCACACGTC TCCACCTCCC CAGTAGGAAA ATTTGTTTAT ATAGACAAAA
11551 CTCAACTGAT TAAAAAATAA AAAAAGAAAT GATACTTACA TTGTCGTGTT

FIGURE 3-4

11601 AAGATACAAA AGCAATAACT TTTTATTGTG AAAATAGTCT GTTTTTGAAC
11651 AATATATTGT TTTGTTTTTT CCTGTGAAAG TTGAGAACT AAATATACGA
11701 AGAGATAATG GTCAGACCAT AAATAAAAAT AGAACTTTGA CTCAAAATTT
11751 ACAGCAGTCT GCCCAGAAAA CCAGCCCTTT ATCTAAAAATA AACAGACCAG
11801 GAAACCAGCC TGTATGTCA GACTTATAGG AAGTCAGGTT GCTATCTCTA
11851 GAGACAATAC ACAAAGCTAT GCAATAACTG CTGTAACAGC CCCAAATGGT
11901 CAGAATTTGA TTAATAACCG ACAGCCCCC TAATTTTTTT CTTCACTNNN
11951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNTTC
12001 ACCGCTTGCT AGAACTGTGG CCTTGGGTCA TGTTATTTAA TGCCTGGAGG
12051 CCTCAAATGT TAACTAGGTA ATGGTAAGAC CTACCCAGTA ACTTAGCATA
12101 AATAGTAAAT TCATTCATTT AATGTTTTCA AACAGTGCCA GACATTGTTT
12151 AATGAACTGG GGATATAGTG GTGAACAACA CTGACAGCGT TCTTCATTGT
12201 ATTCTCAAAA CCTCCCTAT AGTAAGTAGG TCTGTGTGTG TGTGTAGGTG
12251 CATGGGGAAT AAAAAATAAT AAGCAAATAA TGAACAATAA AATTATTTTA
12301 TTTAAAAAAA AAGAAATGAT ACTTACATTG TCGTGTTAAG ATACAAAAGC
12351 AATAACTTTT TATTGTGAAA ATAGTCTGTT TTTGAACAAT ATATTGTTTT
12401 GTTTTTCTCT GTGAAAGTTG AGAACTAAA TATACGAAGA GATAATGGTC
12451 AGACCATAAA TAAAAATAGA ACTTTGACTC AAAATTTTACA GCAGCTGACC
12501 CAGAAAACCA GCCCTTTATC TAAAATAAAC AGACCAGGAA ACCAGCCTGT
12551 TATGTCAGAC TTATAGGAAG TCAGGTTGCT ATCTCTAGAG ACAATACACA
12601 AAGCTATGCA ATAAGTCTG TAACAGCCCC AAATGGTCAG AATTTGATTA
12651 ATAACCGACA GCCCCCTAA TTTTTTCTT CACTTCCAAC TTAGGACGAA
12701 CCAGAGAAAG CTAAATATGC ACCACCTACT AATCAAATAG GGTGCCGCGT
12751 TTCTAATGAA CCTCCTACA GCTTCCCCAG GCCAGCAGCC CCCAATCAGG
12801 AAACGCCTGA AGCCTTCCCT TTTTCTCACT GTAAAGCTTT CCCACTCCTC
12851 TGCCTGGCTT TGAGTCTCTG TCAATACACA AGTGAGGGTG TCTGACTCCC
12901 TTGCTATAGC AAACCTGGGC CAAGTAGATT TTAATTTTCT CATTTGATTG
12951 GTCTTTTATT TCTAGAAGGA ACATACAAGA AAATTTAAAG GGAATCCAT
13001 TCCTAATCTT TCATATTATA GTAGTCCCCT TTTATCTGCA GGCATATTT
13051 TCCAAGACCC CCACTGAATA CCTGAACTG TGGGTAATAT TGAACCTAT
13101 ATATACTCTC TCTATATATA CATATATATA TATATTTTTT AATTTTTTTT
13151 TACTTTATCT TTAATTAGCT TTAGCTCTTT TTTTTTTTTT TGAGATGGAG
13201 TCTCACTCTG TCACCCAGGC TGAGTGCAGG GGTGCAGTCT TGGTCACTG
13251 CAACCTCTGT CTACCGGGTT CAAGCAATTT CTTGTGCCTC AACCTCCGGA
13301 GTAGCTGGGA CTACAGGCGT GTGCCACCAC TTCCTGGCTA ATTGTTTTAA
13351 ATTTTAGTAG AAACGGGATT TCACCAAGTT GGCCAGACTG GTCTCGTACT
13401 TCTGACCTCA AGTGATCCGC CCACCTTGGC CTCCCAAAC TCTGGGATTA
13451 CAGGCGTGAG CCACCATGCG CCCAGCCATA GACTATATAT TTTTGATCTG
13501 ATAAGTGGTT CAGCTACTAA GTGACTAACA GGCAAGTAGC ATCTATAGTG
13551 TGGATATGCT GGACAAAAGG ACATTCACCT CCTGGGCAGG ATGGCACAGA
13601 ATGTTGAGAG ATTTTATCAT GCTACTCAGA ATGGTGTGCA ATTTAAAACT
13651 TATGAGTTGT TTGTTTCTGG AGTTTTCAT TTAATAGTTC AGACCATGGA
13701 TTGACCGCAG GTAAGTAAA CTGTGGAGAG TGAACTGTG GATAAGGGAG
13751 GACTATTGTA TTGTTAAGTC AGACTCATTA GGCAATCATA ACTCTTGATT
13801 TGCCATCAGA AATGCTGCAG AAATATGGGT TAAAAAAAAC TGTTCAAAAA
13851 TAGGGTCAGG GATGTCCTTT AACTTGTTAC TTCCAAAATG TTAGTGAAAA
13901 CTGTGGCCCC AAAGAGTGAA AGGAACAAAT GACTAAGAGA AAATCTTGTT
13951 TTCAGGATGA CAGATTAAAA AAGAAGCAAC TTGCTGAAAC ACTGAAAATC
14001 TCTCCACTTG TAAGATAACA CAAAACCTGGC TAAACTGGT TGAATGAAT
14051 ATGGCCAACT CAAGTCTGCA CAGAACTAAC TTGGTGATGT TACAGCCCAA
14101 ATTTCCACCA CATATTTTAT ACTAACTCCC CCCGGATTTT CACACATGAT
14151 CTGTGAGGTA GCATGAAGAG GTAACTATGC ATGCCTAAGG ACTTGGGAGA
14201 CCTCCCCATT TCCTTCACCT AATCACCAC TAATCCCAGA ATCCGCCCCC
14251 AAACCTTTTC TATAAAGCCA CTTAAAGCCA GCATAGGGAG ACAGATTTGA
14301 GCTGGACTCC TGTCTTCTTG TGGGTCACCT TGCAATAAAA AGCTTTTCTT
14351 TTCTCAACAC CTGGTATTAT AGTATTGACT TCTAGTTCAT CGGGCAGCAA
14401 GCCCCTTTTG GTCGGTGACT ATTCTTGTTT GCTGATATTT CCATTGGCCA
14451 AAATATAAAC CTCTTAGATG AAACCTCAGT ACGTAAATGG CGCCACAGAA

FIGURE 3-5

14501 TGCTGTGACA TTTTCTCTT GGATTATAGC AGGTTACTTT ACTGAATACC
14551 GTAGGCAGTT ATAACACACT AAGTATTTGT GTATCTAAAC ATAGAAAAGA
14601 TACAGTAAAA ATATGGTAAT TTTTTC AAC TTTTAGTTGA GATTTGGAGG
14651 GTATGTGCAC ATTTGTTACA AGGGTATATT GCATGATGCT GAGGTTTGGG
14701 GTACAATTGA ACCCTGTCAC CCAGGTAGTG AGCATAGTAC CCAATCGATA
14751 ATTTTTC AAC CCTTGTCCAT TCCCTCCCCG TTCTTGTAGT CCCCAGTTTC
14801 TGCTTTTCCC ATCTTTATAT CCGTGTGCAC CCCATGTTTT GCTCCCATGT
14851 GTATGTGAGA ACTTGTGGTG TTTGGTTTTT TATTTCTGCG TTGATTGCT
14901 TAGGATAATG GCCTTCAGCT GCATCCATGT TGCTGCAGAG GACGTGATTT
14951 TATCTTCTT TATGGCTGTG TAGTATTCCA TGGTGAAAAA TATAGTACTA
15001 TAACCTTACT AAATCACTGT CATATATATG GTCTATCATT GACTGAAATG
15051 TATACAGTGC ATGATATATA TATATATATA TCTATAATGT CTTATCCATT
15101 TCGTGTATTA TGAGATTTGA TTGCTAATAT TTTATACAGG AGTTTTGCAT
15151 CTTTTTCACT AGTTGACATT GCTTGTAAAT TTCCTTTTTT TGTGATGTCC
15201 CTGTTAGGTT TTAGAATCAA GTGTATACCC GCCTCATAAA ATGGGTTGGA
15251 AAATGTTCCC ACCCTTCTG TTCTCTGGAA AATTGGTGTT TTTTCTTAA
15301 AGTTTGGTAG ACATTATTGT TAAAACCATG GGGTCCCTCGA TTTTCTTCA
15351 TGGAAATTAC TTCAAATTAC ACTTTAAATT TCTTTAAAT CTGAGTATAG
15401 GGCTATCAGA CTTTCTGCTG TCTTATGTCA GTTTTTAATA AGTTGTTTTT
15451 GTAGGCGTTT GTTATCTCAC TTTCATATTT TTGATATAAA GCTTTTCATA
15501 ATATCATTA TGTCTATAGT GTCTAGTAGT TTCCATCTTT ACTTTCTGAC
15551 ATTGGTTATT TGCCAGTTTT AGGAGTTTAT CAATTTTATT AGTCTTTTCA
15601 AAGAACCATC TTTTGGCTTT GTTAATCCTC CCAATGGTGT GTTTCTTTTC
15651 TCATTACTTT TTGCTCTTTA TTTCTTCAA CTTCCTTTTT GCTTAATTTT
15701 AAAATAATTT CTTGAGATTG AGATAAGCCT CAATGATGGG TCACCGATTT
15751 CCAGTCTTTC TTCTTTTCTA ATTATGCATT TTAAACCAGA AATCTTTCTC
15801 TAAGTGTAGC TTTAGTTGCA GCTCACAAGT TTCAGATCTG TCTCTCAGTC
15851 TGGAGGTTGG AGATCTGACC ATGACCATGA AACCATCCAG TCACAATGTG
15901 GCATTATTTT TTTAATTTTT TTTTTTTTTT TTGAGATAGA GTTCACTCT
15951 TATTGCCCTAG GCTGGTGTGC AATGGTGCGA TCTCGGCTCA CAGCAACCTC
16001 CACCTCCAG TTCTTTTGCC TCAGCCTCCC AAGTAGCTGG
16051 GATTACAGGC ATGCGCCACC ATGCCCAACT AATTTTGTAT TTTTAGTAGA
16101 GATGGGGGTT CTCCATGTTG GTCAGGTTGG TCTTGAAGTC CCGACCTCAG
16151 GTGATCCGCC CACCTCAGCC TCCCAAAGTG CTGGGATTAT AGGAATGAGC
16201 CACTGTGCCC GGCCCAACTT GGCATTATTT ACCCAGAAGA GCATGACCAT
16251 GAGAACAGTA GAATTTGTAA GCTTTGAGTG GGTGACTATG AGTGTCTATA
16301 TAGGTAGATA GGTTATATTT TGGGTGGTGG TAGGAGAGGG CTTACAGTTT
16351 GCTATGACAG CTTTTTATAT GGATCATCCT TAGTAAAAGA TTATTTAATT
16401 TTTGAAATCA AAGGGGAAAA CACTAGTTTA GGCTTCTTCT TTTCTTCTT
16451 TTTTAGAGAC AGGGTCTTGC TCTGTCACCA GGTTAGAATG CAGTGGTGCA
16501 ATATTGCTCA CTGTAACCTC AAATTCCTGG GCTCAAGTGA TCCTCCTACC
16551 TCAGCCTCCA AGTAGTAGT ATTTACAGGC ATGCACCAAC ACATCTGGCT
16601 AATTTTAAAA ATTTTTTATG GAGATGAGGT CTCACATATG TGTCCAGTCT
16651 GGTCTTGAAT CCTGACCTCA AGTGATCCTC CCCCATCAGC CTCCCAAAGT
16701 GCTGCAATAT TTTAAATCCT GTGGTAGGTC AAGTGGTTGT CTTCTATCTT
16751 GGGGTTTATA AAGTACATGT CAAGAAATTT AGGGTATGGT TAGATTAGCT
16801 TTAATAATGT CATGTTTTAT AAAAATCAAT GCATCATTTT TCTGATTGAA
16851 AATTTAACAC AAGACTCAGA ATCTTTTTGC AGTAGTGGAA TTAATTTTAT
16901 TATAGATCTT TGCGATAATG AATGATGATA CATCTGGCCA AAAATAGGTA
16951 CTATAGTCTT TTAGGAAAAC AGCTAATCTG CTTGAAATAT GTGTAGAAAT
17001 AATTTAGTGC ATCAGCCCAT ATTGGCAATA ACTTCTCTCT AATTTTTTTT
17051 TATAGAAAAT TTTTACTACT GGAGATGTCA ACAAAGATGG GAAGCTGGAT
17101 TTTGAAGAA TTTATGAAGTA CCTTAAAGAC CATGAGAAGA AAATGAAATT
17151 GGCATTTAAG AGTTTAGACA AAAATAATGA TGGTGTGTCT TTCTTTTGTA
17201 TTTATCACCA GCTATGAAGA AGCATTTATC ATGCTTTCAA GAGTCTAAAA
17251 GGATGCTTAT TTAATCTCTC TGGTTTTAGA TGATAATTAT TATTTGTGTT
17301 AATACTTTTT TTTAGTAATG TGATTTTTAT GTAGAGTTTA TATTATTTAG
17351 TGAAGAAAAA TTATAGATAG CTTTTCTTTT TCATTACTTT GAAATGTAAT

FIGURE 3-6

17401 GAATTACATT TCTGAATTAA AAACGTGTGG CAGGGCCTGT TGTAATGTT
17451 AACTATGGAA CATTATGCTG ATTTGAGTTA AACCTGTAGG TTAAAAATAA
17501 TAATTATATT TTCTTGTCCT CTGGGTAAAA TGAGATTTCT TTTTATTTGT
17551 ATAGAAGAAT GACAGTTGTG TCATCTAAAA TTTAAAAAAC TTTCAGATTA
17601 TCTTGCACTCT GTTAGTTTTT TTGGAAGAAT TAATTTAGAG AAGATATCTC
17651 TGATCCTGGA AATTAGGGAA AAATAGCATA TAAACGTTTA AGTGTGTACC
17701 TTCTGGTTAA GATTATGACT TCTATATTTT GATTAATAGG TTGGAGTTTG
17751 TCTTAATCTG TTTTCTGTTG CTGTAATGGA GTACCACAGA CTGGGTAATT
17801 TATGAAGAAA TGAAATTTAT TTCTTATAGT TCTGGAGGCT GGGAAAGTTCA
17851 AAGTTGAGCC GAATCTGGTG AGGGCCTCTT ACTATGTCAT AACATGCTAG
17901 CAGGCATCAC AGAGCAAATG CACTACCTCA GATCTCTCTT CCTCTTCTTA
17951 AAAAGCCACT AGTCCCATCA TGGGGGCCCT ACTCTGAAGA CCTTATCTAA
18001 TTCTAATTGG AAATAGGGTC TTGAAGCCCT CATCACTAGA GGTAACCTTT
18051 AACAGGAAGA GAGAATTTAT AAAAATTATA ATGCAGCACC AAATCCCTCC
18101 CTACTTGTGA ATAGTCAAGG TCATTTTATT TACAGACTTG TTATTAAAGA
18151 AACAGTTAA ACAAAATAGT TGAGAGGAAA TGTGGTTCAT GTCTGAGATC
18201 AGCAAACCTT TTTGTCCAGA AGTCCAGATA ATAAATATTT TAGCTTTGTG
18251 GGTCACTGGG TCTCAGTTGT AGCTACTTGT CTCTGCTGCT GTACCTCAA
18301 AGCAGCCATG GATAATATGT AAATGAATGG GGATGACTGA TTTCCAATAA
18351 AAACCTTTAT TACAAAGATA GTTAATACAC CTTATTTGGC TTGAGGGTTA
18401 TAGTTTGCCA TCCCCTGATT TACAATGAAT ATTAAGTTT AATTCAAAGC
18451 AAGTTCCCTC AAACAAACAA ACTAACTCT AGATGATTTT GAAGATTATT
18501 CACATCTGTG ACTCTCAGCC AGGAAGAGCT GAGTTTGGGT TGGAAAGTAG
18551 TACTATTGGA ACATTTGTTG CCCATAAGCC TTACAATATA TGCCCCTAAG
18601 TCTAGCCTTA GTCCAGTCTT CTAGCAAAAC TCAGTTTTCT TTCTTCTCTG
18651 CAACTTTTCA TTCCAACATC GACCCTCTGC AGTTCAGATT GTCTTGCAAG
18701 TCAGATTGTC TGTGTGCTGC TATGGTAGGC AGTAGCTGAG AGATGGAGCT
18751 ACCTTAAGAT CAATTGCCAG ATAATCAGAG GTCAATTATC CCAGTGCATA
18801 AGTAGTGAC ATATCAATTG TTCATTTTAT AAAATTCTAA ATGAACCAGA
18851 GGCAATAATT AAAGATGAAA TTTTGATGGT ATATTGTAG GAAATCTACA
18901 CAATGTTTTCC CAAATTTCCC ATGTTTGTGT ATTTTAAAC AATGTGGCAT
18951 TATTGGTTCA TATTTTATT TTTTAGACTT CCTTAATGCA AAACATATAC
19001 AGTTGATCCT CATTATTTGG GGATTCTGTA TTTGCAAATT TGCCTACTCA
19051 ATAAATTTA TCCCCAAAGT AACCCCAAAA TATATACTCA CAGTACTTTC
19101 CCAGGCATTC ATGGACATGC ACAGAGCAGT GAAAACTTG AGTTGCTCAG
19151 CATGTACATT CCTAGCTAGT AGAATAAGGC AATACTCTGC CTTCTTGTTT
19201 CAGCTCTCAT ACTATTAAC AGCAAGTATC CCTTCAAGG TCTATTTTGT
19251 GCCAGTTTTT GCATTTTGT ATTTTGTGT GTAATTTCTT TTTTAAATG
19301 TTCCCCAAAG GTAGTGCTGA AGTGCTGTCT AGTGTTCTTA AGTGCAAGAA
19351 AGCCATAGCA TGCCTTATGG AGAAAAATA TGCGTTGGAT AAGCTTTGCC
19401 CCAAATTCAT TGTTAGTGAA TCAACAGCAC ACATTAAATG AGGTGCCTTC
19451 AAACAGAAAC AGACATAAGA CATGGTTATG TATTAATCAG TTGATGAAAG
19501 TGTTGTAATC AGAGGCTCAC AGGAACCTAA CCCTGTTTTT CCTGTAGGAA
19551 CAATGGTTTG GTATTTGCTA ATTCAGTGTT TGCAATGAAT ATAGAATTTT
19601 ATGGAAGATG ATTGCTGTGA ATAATGAGAA TTAACCATAT CTCTTAAGA
19651 GTGCATTTCT AAAGGAGAAT ATTCAGAAGG GTATTTGCAT AATTTCTTTA
19701 CTAACAGATG CTGCCTCTCA CTGTCCTTAC ATGGTCCAGA TTCTCATGCT
19751 GCTCCTTCCC TCTCCCCAGG AGGATTCTCT CAGAATCCTG TCATCTCCTC
19801 CAGGGTCCTT TCTCCAAGAA AGTCTATCCT TTCACACTA ACAGTAATTT
19851 TGGTCTTCTT CTTTTTCTGG AGAAGTCAGC TGTTTATGCT GCTTCAGCAC
19901 CAGACCTCTT CTACTTTGT TTTGTTTCAT TCTTTTTCAT GTACAGTAGT
19951 CTTAGGATTC TCATGAGCCT GTGAGCTGCT AGAAGGAAAT ACAGCAGTGC
20001 TTACATTTAT TGCTTCTATT TTATTTTCTA TTTTCTCTC CTGTCTTCTG
20051 ATTGTTCTCC TTCTGTCCAC AAACATGCTC TAATTTCCCT AGTATTAAAA
20101 ATTTTCTGTC TTTTGTGTT CTTTTATCCT TGCTCCCTTA TTTTFACTGC
20151 CAGATTTTTA TTTTATTTA TTTATTTTGG AGATGGAGTC TCACTCTGTC
20201 ACCCAGGCTG GGGTGCAGTG GCGCGATCTC AGCTCACTGC AACCTCCGCC
20251 TCCCAGCTTC AAGCAATTTT CCTCTTTTAG CCTCCAAGT AGCTGGGATT

FIGURE 3-7

20301 ATGGGCACCT GCCACCATGC CTGGCTGATT TTTCTATTTT TAGTAGAGAC
 20351 GGGGTTTCAC CATGTTGGCC AACTGCTCT CTAAGTCTG ACCTCAGGTG
 20401 AACCAACCCG CTCAGCCTCC AAAAGTGCTG GGATTGCAGG TGTGAGTCAC
 20451 TGTGCCTGGC CTTTTACTGC CAGATTTTTA AAAGAATAGT CTGTGCTTTA
 20501 GCTCTATTTT CTCATTTACT ACTTCTCTTT AACTCAGTCA TATATGATGT
 20551 TTTGCATAGT AAATGTCTAG TAATTTATTA AAAATGTAGA AATAGGTACT
 20601 TTTAAAATGA ATAGATCCTA CTTTAATTGA ATTTATCTTG GAGTTAGAAT
 20651 ATCTTGATTT GGATTTTAGT TCTGCTACTT CTTAATTACA TTAATTGGTA
 20701 AGGCCACTTG TGAAGTCAGT CTCTTTGGAG GAATATTATT TATCTATAAG
 20751 GCTGTTACAA TTAAGTAATT TTAATAAATG TGTATTTATT TTTAATGTA
 20801 TTTGTTACAT TTTTAGTATT GATGTTGGGA TAGGCATTTA AGCAAGTCTA
 20851 TAACTCACCT ACATGCATAA TTTTGCCTTA ATCAGTTTAA AGCTTTCTCT
 20901 TAAATGAGAG ATTTGAAATT CATAATTTCT GTGGTTCTTA TCAGTTCTGA
 20951 GTTTTATTTT TTGCCCTTTT TATTTTTTTA AAGGAAAAAT TGAGGCTTCA
 21001 GAAATTGTCC AGTCTCTCCA GACACTGGGT CTGACTATTT CTGAACAACA
 21051 AGCAGAGTTG ATTCTTCAAA GGTAAGCTCT TCATGTTGGT CAACAATTGA
 21101 CTTTCACTTT AATATCCTGC ATTAGAACTC TGTGTTTGTA AGTGTGGCTT
 21151 TAAAAACACT CCCTAGTCTT CATTATGTAT ATCCAAGATC TTTTGTCTT
 21201 TTTTCCCTCC TATCTTTTG TATGTGTACA TTTATCTAAA GTGTAAGAAT
 21251 GGGAAAGTGA AGCTCAGACT GGACTCTTTC TTTCAAGGCC TCAAAGGATA
 21301 GTGGAATGGC AGGAAGTAAG GTTTTAACTC CATAGATGAG GAGCTGAAGA
 21351 GTTTTGGTGT TGCTTTTTCT CCATTTGATT TCTAATGTGA CAGTAAACT
 21401 CATTGATTCA AACTAAGAAG ACTAGCAGAT TCATCACATT ATTTAACCTA
 21451 GATGTGACTG GAAAAAAGGG AAATTAATAA GCTCTCCAAG CTAACAAAGA
 21501 AATACCTGTT TAAACTTTCA GAAAACAGAA ATGCAAATTT GAACCTTATT
 21551 GTCTGGGGCA ATCAGTTTGA CTATTTAAGT CAGACTTTTA TACTCTTAAT
 21601 GTTTTGTTC ATGGGATAGA GCAGTAATCT CTGCAGCCCA GGTGCTCTCA
 21651 AATACTCTGT TGCTATAAAC ACAGGGCAGG AACTGATTTT TTATGATAAC
 21701 GTAAACAGA AAAGGACAAT TATATTGTAT TAATATTGTT GTGAATATT
 21751 TCAGTCTCA CATTGTCTAA AAATCTTCT AAATGGCTTT GTTATTGAAT
 21801 TTATCTCATT TTATCTCTGT GCCAACAGCA TTTTCATCCT TTCTCTTCAT
 21851 AATTTCTTTT ACAAACAGCT GCTCAAGAGG AAGGCTCAAA GTCTCAAGGC
 21901 TGAGCACGTA ATGACTTTTG TTAGTACTAG ATGAGAAGGG CTTTCTGAG
 21951 GAAATGAAAA CCTAAAACAT GAAAAGAAGA TAAACAGAAT TTGGACAGTG
 22001 AGATATAGAG CATATAATAT TCTGCTTCTA AAGTAATATT CTTCTAGGAA
 22051 AGTGAGGGCG TTTCCCTGGC TGTTAGGCCA GAAATCATAT TCCTATATTT
 22101 TCTTTGATAG CTTTAGGAAT AATGCAAATT CTAAGCCCAA GCTTCAGAAT
 22151 AGACTAAGAA GTATTAGCTT AGCTGCCATG ACAAATACC ATAGGCTGGA
 22201 TGCATTAAAC AATGGAAATT TAGTTTTTCA CAGGTCTGGG AGCTGGGAAG
 22251 TTTAAGATGA GAGTGCCAGC ATGGTTGGGT TGTAGTGAGG GCTCTCTTC
 22301 TGGCTTGACG ATAGACCCCT TCTCACTGTA TTGTCATATG GCAGAGAGAG
 22351 AGAGAGAGAG AGAGAGAGAG GATCTTTCTC TTGCTTTCTA
 22401 TTATAAGGCC ATAGTCCTGT TGGATCAGGG TTCCATTCTT ATGACTTTAT
 22451 TTGACTTTAC CCCCCTAAGA TGCTATCTCC AGATATAATC ACACGGTGGG
 22501 TTAGGGCTC AACATTTGGA TTTGGGAGGG ACACAGCTCA GTCCATAGCA
 22551 AAGGATAATG CAGAGGGTTG GATATTTAAA AGTAGCTACA CAATTTTAA
 22601 TATAAATATT TTATGGTAAC TTTTTTTTTT TTTTGAGATG GAGTCTAGCT
 22651 CTGTTGCCCA GGCTGGAGCG CAATGGTGCG ATCTCAGCTC ACTGCAACCT
 22701 CCGCCTCCA GGTTCAGCA ATTCTCCTGC CTCAGCCTCC TGAGTAGTTG
 22751 GGACTATAGG CACGCGCCAC CACGCTGGC TATTTTTTTT TTATTTTAC
 22801 TAGAGACGGG TTTGCACCAT ATTGGTCAGG CTTGTCTCGA ACTCCTGACA
 22851 TCAGGTGATC CACCCATCTT GGCTCCCAA AGTGCTGGGA TTACAGAAGT
 22901 GAGCCACCGC GCCTAGCCAG CAGCTTTACT GAGATGTAAT TCACATGCCA
 22951 TAAATTTACT TTTCTAAAGT ATACAATTCA GTGACTTAAA ACATTTATTT
 23001 ATTTTTAAAT TGACAGAATT ACATGTATTT ATCATGTACA ACATGATGTT
 23051 TTGAAGTATA TGTACATTGT GGAGTGACTA AGTCTAGCTA ATTAACATGA
 23101 TACATCTCAT ACTTAATGAT TTCTGTGGTG AGAACACTTT ACATCCATTC
 23151 TCTTAGTATT TTTCAAGAAT ATAATATATT ATTATTAATT GTAGTCTTCA

FIGURE 3-8



23201 TGTGTATAG TGGAGCTCTT GAACTTATTC CTCATGTCAA GCTGAAATTG
23251 TGTGTCCTTT AACACAAACC ATACCCGACT CCCAAAGTAT TCTGCTCTCT
23301 GCTTCTATGA GATTAACCTT TTCTGATTCC ACATGAGTGA GATCATGCAG
23351 TATTTATTTG TCTTTACCTG GCTTATTTCA TTCATATTGT TACAGATAAC
23401 AGGATTTCTT TCTTTTTTTA ATGGCCGAAT AGTTTTCTAT TGTATATGTA
23451 TAGCACATTT TCTCTCTTCA TGCATTGGTG GACACTTAGG TTGATTCCGT
23501 ATCTTGGCTA TCGTGAATAG TGCTATAATG AACATGGGAA TGCACATGGC
23551 TCTTTGACAT ATTGATTTCA TTTTATATAT GTGTATATAT ATATGTATAC
23601 ACACACATAC ATACAGTGGT GGGATTGCAG GATCATATGG TAGTCTATA
23651 TTTAATTTTT AAAGGAACTC CATACTGCTT TCCATAATGG CTGTATTAGT
23701 TTAACCTCTC ACCAACAGGG TGCAAAAGTT CCCTTTTCTC TACATACTTG
23751 CCAACACTTG TTATCTTTTG TCTCTTTGGT AATAGTCATT CTAAGTGTAG
23801 TATGAGGTGA TATCTCATTG TGGCTTTTAT TTGCATTTCT GTGGTAATTA
23851 GTGATATCGA GCTTTTTTTT TTTTTTGAC TTTGGCCATT TGTATGTCTT
23901 TGAAAAATGT CTATTGGGGT TTTTGGTTG TTTATTGAG GTTTTNNNNN
23951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24251 NNNNNNNCCG GGGTTCCCGT CATTCTCCCT GCCTCAGCCT CCCCAGAGTA
24301 GCTGGGACTA CCAGGGCACC CGCCCACCAC GGCCCGGGCT AATTTTTTGT
24351 ATGTTGAGTA GAGACGGGGT TTCACTGTGT TAGCCAGGAT GGTCTTGATC
24401 TCCTGGCCTC GTGATCTGCC CGCCTCGGCC TCCCAGAGTG CTAGGATTAC
24451 AGGCGTGAGC CACCGCGCCT GGCCTGATTT CTAGTTTTTT ATTATTGTGG
24501 TCGGAAAAGA AACTTGATAT GATTTTCATTC TGCTTAAATT TGTTAAGACT
24551 TGTTTTGTGG CCTAACATAT GATATCCCTT GGTGCATGTT CCATGTGCAG
24601 TTGAGAAGAA TGTGTATTCT CTTGCCATTA GGTGAAATGT TTTATGTCTG
24651 ATCTGTCCAT TTGTTCTAGA GTATAGTTTA AGTCTGATGT TTCTTACTGA
24701 TTTTCTGTTG AGATGATTTG TCTATTGCTG AAGGTAGGGT GTTGAAGTCC
24751 CCTACTATTG CTGTATTGCA GTCTCTCTCT CCTTTCAGAC GTATTAATGG
24801 TTTTTATTTT ATTTTATTTG TTGTTGTTGT TGTGTTGTT GTTGTTTTTG
24851 AGACGGAGTC TCACTCTGTC ACCAGGCTGG AGTGCAGTGG CAGGGTCTCG
24901 GCTCACTGCA GCCCCCGTCT CACGGTTCAA GCGATTCTCC TGCCTCAGCC
24951 TCCCAGATCG CTGGGACTAC AGGCGCATGC CACCACGCCC AGCTAATTTT
25001 TGTATTTTTA GTAAAGACGG GGTTTCACCA TGTTGGCCAG GATGGTCTTG
25051 ATCTCTTGAC TTCATGATCC ACCCGCCTTG GCCTCCCAA GTGCTGGGAT
25101 TACAGGTGTG AGCCACCACC CCTGGCCAAT GTTTGGTATT TATCTTTAGG
25151 TGCTCTGATG TTGGGTTTCA ATATATTTAT AAAAAACAAT AGCTACATAA
25201 CTTATTAAGG GATATGCAAT ATAAAAATA TAAATTGTGA CACTGAAAAT
25251 TTAAAAATGG AGGAGTGGAG TAAAAATACC TTATATAAAC TTACTATTAT
25301 ATCCTCTTAT TGAATTGACC CTTTTATCAT TATATAGGAA CTTTGTCTCT
25351 CCTTTACAAC TTCTGACTTA AAGTTTGTTT TATATGATAT AAGTAAAGTT
25401 ACTCCTGCTC TCCTTTGGTT TCTGTTTCCA TGGAATATCT TTTTCCATTC
25451 CTTACCATC AGTCTGTGTG TATTTTTACA GATGAAATGA GTCTGTCATG
25501 GGCAGCATAT AGTTGGATCT AGTTTTTTTA ATCCAATCAG AACTGTGTT
25551 TTTTGATTGG ATAATTTAAT CCATTCATGT TCAAGGTAAT TATTGATAAG
25601 TAAGGACTTT GTACTACCAT TTTGCTTATT GTTTCATGGT TCTTTTATAG
25651 ATCCTTTATT CTTTTCTTCC TCTCTTGCTG TCTTTTTTTT GTGGTTAAGT
25701 GATTTTCTCT AGTGGTATGT TTTGATTTCT TGCTTTTTAT TTTTGTGTA
25751 TCTCCTATTG GTTTTTGGTT TGTGGTTACC AAGAGGTTAC AAAAAACATC
25801 TTAAGAGTTA TAATAGTTTA TTTAACTTG ATAACCTAAT TTTTATTGCA
25851 AAAACCCCCC AAAACAAAAA AATCTACACT TTTACTTAAT CCCCTGAAAT
25901 TTTGAATTTT TGATGTCACA GTTTACCTCT TTTCATATTG TGTATCCCTT
25951 AAATTATTGT AGCTATTATT ACTTTTAATA GTTTTCTCTT TCCTACTACA
26001 GATGTAAGTG ATTTGCATAC CATCATTACA GTATTATTTT GAATTTACCT
26051 GTGTACTTTT TTTTATCAGC CAGTTTATA CTTTCAGATG TTTTGTGTT

FIGURE 3-9

26101 ACTCATTAGC ATCTTTTTCT TTCAGCTTGA GGAGCTCCTT TTACGTTTCT
26151 TATAAAATAG GTGCGGTCAT GATTATCTCC CTCAGCTATT GTTTGTCTGG
26201 GAAAGTATCT CTCCTTCATT TCTGAAGGAC ACTTTGCTGG GTACATTACC
26251 CTTGGTTGGT ATTTTTCTCC TTGAACGCTT TAAATATATC ATCCCTTTCT
26301 CTCCTGACCT GTTAGGTCTC TGCTGACCAG TCTGTTTCCA ACCATATTGG
26351 GACTGTCTTA TATGTTATTT GCTTCTTATC TTTTGCTGTT TTCAGGATCC
26401 TCTCATTGTC TTTGATTTTT GATAGTTTGA TTGTAATATG TCTTGGGGTA
26451 GTCTTGTTTG GATTGAATCT GATTAGAGAC CTTGGACTTT TCCTGCATGT
26501 AGATATTTAC CTCTTTCTCC AGGTTTGGAA AATTTTCTGT TACTGTTTCT
26551 TTAATTAAGC TTTTACCCC TTTTATCTTC CTTTCTCCTT TCTTCAACTC
26601 CTGTGACTCA AAACCTTGCT CTTTGTATGC TGTTCATAA ATCTTGTAAG
26651 CTTTCTTCAT TCATTTTCAT TCTTTTTTCT CCTCTGTGTA TTTTCAAATA
26701 ACCTGTCTTT GAGTTCATAG TTTCTTTCTT CTTCTTGATC ACTTCTGCAG
26751 TTGATGCTCC CATATTGCAT TTTAATTTTG TTCATTGTAT TTTTCAGCCC
26801 CATGATTTCT GTTTGATTTT TTCTTTTATT ATTTTCATCTC TTTATTACCT
26851 TTCTCTTTGT GGTCACTCGT TATTTTCTTA ATTTCAATTGA ATTGTTTCTT
26901 TGTATTTTCT TGAAGTTTGC TGAGCTTTCT TTGAATTCTA TGTCAATTCA
26951 TACATCTCTG TTTCTTTAGG GATGGTCGCT GGTACTTTAT TTTGTTTCTT
27001 TAGTGGTGTC ATTTGTTTCT GATTGTTGTT GATGTTTGTT GCCTTGTTGT
27051 TACATCTGTG CATTTGAAGA AGTAGGCACT TATTTCAATC TTTGCAGACT
27101 GGCTTTGTCT GAGAATGCCC TTCAACAGTC AGCCTGTCTA GAGATTCTTT
27151 AATATTTAAT TAAATATCTT TAATATTTTG AAGAACTTCC AAATTGTTTC
27201 TAAAGTGGCT GCACCATTTT ATAATCCCAG CAGCAATGAA TGAAGGTTTC
27251 AGTTTCTCCA TAGCTATATG AATACTCATT ACTGTCTGTC TTTTCATTTT
27301 TTGATTTTTTA TTTTTTTTTT GAGAAAGGGT CTTGCTCTGT CATCCCATCT
27351 GGAGTGCAAT GGCACAATCA TGGCTCATTG CAGCCTCAAC TTCCCTGGCT
27401 CAATTGATCC TCTCACCTCC TGAGTACCTG GGACTACAGG CATTGTACCA
27451 CAATGCCTGG CTAATTTTTA TATTTTTTGT AGAGATGTGG TTTTGCCATG
27501 TTGCCCTGGT TATTAGTCCA TTCTCATGCT GCTATAAAGA ACTGCCTGAG
27551 ACTGGTAAAT TTATAAGGA AAGAGGTTTA ATTGACTCAC TTTTGCTTGG
27601 CTGAGGAGCC CTCAGGAAAC TTACAATCAT GGTGGAAGGG GAAGCAAACA
27651 CGTCTTCTT CACATGATGG CAGGAAGAGC AGTGCCTAGC AAAGAGGGAA
27701 AAAAACCTT ATAAAATAAT CAGATCTCAT GAGAAGTTAC TCACTATCAT
27751 GAGAACATCA GAATGAGGGT AGCCTCCTCC ATGATTCAAT TACCTCCAC
27801 TGGGTCCCTC ACGTGACATG TGGGGATTAT TGGAATAATA ATTCAAAATG
27851 AGATTTGGGT GAGGACACAG CCAAACCATA TCATTTTTGC CCTGGTCCCT
27901 CCCAAATCCC ATGTTCTCAC ATTGCAAAAC ACAATAATGC CTTTCCAGCA
27951 GTCCCCCAGC GTCTTAACTC ATTCCAGCGT TAACCTAAAA GTCCAAGGTT
28001 TCATCAGAGA CAAGGCAAGT CCCTTCTGCC TATAAGCCTG TAAAATCAAA
28051 AGCAAGGTAG TTATTATACT TCCTAGATAC AATGAGGGTA CAGGCATTGA
28101 TTAATATAC TTGTTCCAAA TGGGAGAAAT TGGCCAAAAT GAAGGGGCTA
28151 CAGGCCCAA GTAAGTCCGA AATCTAGTGG AATAGTCAAA TCTTAAAGCT
28201 CCAAAATGAT CTCCTTTGAC TCCACATCAC ACATCCAGCT CATGCTAATG
28251 CAAGAAGTGG GCTCCCATGG CCTTGGGCAT CTGCACTCCT GTGGCTTTTC
28301 AGGGTACAGA CCCCCTTCTG GCTCTTTTCA CAGGCTGGCG TTGAGTGTCT
28351 GTGGCTTTTC CAGGTGCATG GTGCAAGCTG TCGGTGGATC TACTATTCTG
28401 GGTACTGGAG GATGGTGGCC CTCTTTTTCAC AGCTCCACTA GGCAGTGCTC
28451 CAGTGGGGAC TCTGTGTGAA GGCTCCAACC CCACATTTCC CTTCTGCACT
28501 GCCCTAGCGG AGGTTCTCCT CAAGGGCTCC ACCCTGTCAG CAAACTTCTG
28551 TCTGGACATC CAGGCATTTT CATACATCCT CTGAAATCTA GGCAGAGGAT
28601 CTCAAACCTT AATTCTTATC TTCTGTGTAC CCGCAGACTC AACACCTTGT
28651 GGAAGCTGCC AGGGCTTGGG GCTTGACCTT TCTGAAGCCA TGGCCTGAGC
28701 TGTACCTTGG CTCCTTTTAG CCATGGCTGG GATGCAGGGC ACCAAGTCTT
28751 GAGACTGCAC AAAGCAGCAA GGCCCTGGGC CTGGCCAGG AAACCATTTT
28801 TTCCTCCTGG CCTCTGGGC CTATGATGGG AGGGCCCTTC CTGAAGACCT
28851 CTGAAGTGCC CTGGAGGCAT TTTCCCCATT GTCTTAGTGA TTAACATTTT
28901 ACTCCTTGTT TCTTATGCAG ATTTCTGCAG CTGGCTTGAA TTTTTTCTC
28951 AGAAAATAGA TTTTCTTTT CTGTCACATC ATCAGGGTGC AAATTTGACA

FIGURE 3-10



29001 AACTTTTGTC CTCTGCTTCC TGTGGAATGC TTTGCCACTT AGAAATTTCT
29051 TCTGCCTGAT ACCCCAAATC ATCTCTCTTA GGTTCAAAGT TCCACAGATC
29101 TCTAGGGCAG GGGCAAAAAG CCACCAGTCT CTTTGCTATA GCATAACAAG
29151 AGTCATCTTT GCTCCAGTTC CCAACAAGTT CCTCATCTCC ATCTGAGATC
29201 ATCTCAGCCT GGACTTCATT GCCCATATTA CTGTCAGCAT TTTGGTCAAA
29251 GCAATTC AAC AAGTCTCTGG GAACTTACAA ACTTTCCAC CTCTTTTGT
29301 CTTCTGAGCT CTCCAAATTT TTAAGAAGTT CCAAACCTTC CCAGTCTTCT
29351 TCTGAACCTT CCTAACTGTT CCAACCTCTG CCTGTTACCC AGTTCCAAAG
29401 TCAGTTCCAT ATTTTGGGT ATCCTTATAG TAGCACCCAA CTCCTAGTAC
29451 CAATTTACTG TATTAGTTCA TTCTCAGCT GCTATAAAGA ACCACCTGAG
29501 AATGGGTATT TTATAAAGGA AAGAGGTTTA ATTGACTCAC AGTTTCGCGT
29551 GGCTGGGGAG GCCTCAGATA ACTTACAGCC ATAGCAGAAA GGAAGCAAA
29601 CATGTCCTTC ACATGGTGGC AGGAAGAAGA AGTGCTGAGC AAAGAGGGAA
29651 AAGCCCTATA AAACCATCAT ATCTCGTGAG AACTCACTCA CTATCATGAG
29701 AACAGCAGCA TGGGGTTGAC CACCCCCCAT AATTCAATTA CCTCCCACCA
29751 GCTGTCTCCC GTGACACATG GAAATTATGG GAACTACAAC TCAAGATGAG
29801 ATTTGGGTGG GGACACAGCC AAACCATATC ATCTAGGCTG GTATCGAAAT
29851 CCTGGGCTCA AGCAATCCAC CCACCTTGCC CTACCAAAGT GCTGGGATTA
29901 CAGGCATGAG CCACCATATC TGAAGTGTCT TTTGATTTCT TTTGATTTTA
29951 ACCATCCATT GTTCTGCTT CTCTAGATAA CCCTGACTAA TATATAATTG
30001 GTATGAAGTG ATATCTCATG GCTTTGATTT ATATTTCTTT CATGGCTAGT
30051 GACTTTTTTT GTACTTTTGG GATATTGTTA TTATTATTAT TATTATTACT
30101 AGTGTTTATA CTTCTTCAGT AAAAGTGTTA GAAACAATTT TTAAAGGCAG
30151 AATGTGACCA GAGTTTCCTG TAGTTATATA ACCATCATGG ACCTTCCCTC
30201 AAGTGCTAAG CCATTAGTGT TACTCATGTC ACTCCAAATG TCAGCTTGTT
30251 TTCTTCCATT TCACTGTCTC TTTGTGTCCC AAACCTGAAT TCATGGGAAA
30301 AACATCTGAA TGGTGCTTAA TATGGTTTGG ATATTTGTCC CCTCCAAATC
30351 TCATGTTGAA ATATGACCTC CAGTGTTGGA AGTAGGGACT ACTTGGGTCA
30401 CGAGAGTGGA TCCTTCATTA ATGGCTTGGT AATAAGTGAA CTCTATTAGT
30451 TCATGAAAGC TTGTTGTTGA TAAGAGCCTG GCATCTCATT TCTCTGTCC
30501 TTCTCTCACC ATCTGACACA CTTGCTCACC TTTTTCTTC AGCCATGAGT
30551 AAAAGCTTCC TGAGGTCTCA CCAGAACTG AGCAGATGTT GGTGCCATGC
30601 TTGTACAGTC TGTAGAAGTC TGAGCCAAAT AAGCCTCTTT TCTTTATAAA
30651 TTACCGAGTC TCAGGTGTTT GTTTAAACA ACACAAAACA GACTAACACA
30701 GTGTTGATTG AAACAGCTGT GACTGGGTCA TCAGGGTGTA AGAGAGGAGT
30751 CACTGAGTTG AAATATAGCC TCCTACTTAC ACCTGTTTCA TAGAAGCTGT
30801 AGATATGAAG TAGCTGAAGC AGGCATTCCC TCTGAAACAT GTGTTTCACA
30851 TATGTCATAA TTATCTTCTG CTCTCATTTT TCTTTTAGGC TTTGTCTCC
30901 ATCTCATTTT CCCTGTTTAC TCTCATTTT ATATCTTTAC ATTTCTTTCT
30951 CCAGAATTGT TCAGAAGCTT GGAACCTTC ACTCCAGTTA TTCTTTGACT
31001 ATGCAATTTT TTTCTGTGCT TCATGGCACT TATGGTTTGT AATCCTTGAC
31051 TTGTTTGAT AGCTCAGTGG TTAGGAGTAC AGTTTGGAGT TAGAATGCCT
31101 GGGTTGAAAC TCTTAATTCT ACTCTACTTA CTAGTCTTGT GACTATAACA
31151 AAATCTTAG CCTCTCTTTG TCTGTAAAAT GGAGAGTATA GTAAATACAT
31201 GGGCTTGTTT TAAGGATTAA ATGAGTTAAC ATGTGAAATA CTTAGAACAA
31251 TGCCTGGCAA ATGCTCAATG AATATTGAGT ATTGCTTGCT TTTGTTTAGT
31301 GCCATGCCTG TTGTTCCAC TGAGGGCACA GACCATGTGT ATCTGGTTAA
31351 CAGTTCTATG TCCACCACGT TGCAATAATG GACTCTCAGA AAATATTGAA
31401 GAATATGTTA AAGAATGAGT AGAATTATGC TACTGAAAAG GGTGAGTGGG
31451 AGGTAGGTAG GGGAAAGGAC ATATACAGCC CTGGAGGCAG CATATATGGG
31501 GAATGGGTCA CACAGTGTTC CTTGGTACTC TCTAGACCAT AGTGGGCCAC
31551 CTCTTAGCTA GTGGCCTATG GATTATTTCA GCAGTCTGTT GGAAACATCC
31601 ATGAATATGA TAATAATGAC CCATTTGTGG GTTCTAAGAA AAAGGACAAC
31651 TACAATACTA GACAATAATA GTATGTAAGT TAGGAGGGAA GGGGATGATT
31701 TGTATTAAAC TGTTCTAAAA TTCTTACCTT ATTTAGGATG ATGGGGTCAG
31751 ACATTAACCT TAGACTTTGT TATATATATG TGGTAAAATT TCAAGGTAAA
31801 CCATTGAAAC TGTAGTAGTT GAGTATATAA CTTCCAAATC AGGGGGGAAA
31851 GAAATGGAAT AAGAAAATAA ATACATAAAC ATAAGATTGA AACAAATCAA

FIGURE 3-11



31901 TGAAGAGTAG AGAGAAGAGG GAAAAACATA GAAAGAATGA GATAATTAGA
31951 AAGCAATAGG TAAGATGTGA GAAATAAATT CAAGTACAGT AAAACTCCAC
32001 TAAAAATGTC CCTGCAGTAA TGTTGGGGCA TGATTTCCCT TCATCCCAT
32051 TCTCAAATGG GGCAGCCTAA ATAGCGTTCT TATCCTGTTT CCCTGGGGGT
32101 TTGAGGTGGG TGACGAGTAA GTTAGAAGAT AATCACCTTC TGATCAGTTA
32151 GGACTTTCTC AGTTTAGTCT TCAATTAATA AAAATTAATG TAAATTTTCAT
32201 CAGAAGGCAG AGATTGTCAG ATGAAAAGAAC AAGCAAAATA AAAGTCTTAC
32251 TGAAAAAAG CTGGGGTAGC TATGTTAATA TCAACTGTTA ATTATTATTA
32301 ATAATCTATT AATAATAGAT TATATAGTAA AAACATTAAT AAAAATAGAG
32351 TGCTACTACA TTTTAAATTT CAGTATGAGG ATATACAATT TTTAAGCTGG
32401 TTGATAAAAT TCTGGGGATT AATTGGCAAA TCCATCATAG TGGTGAGAGA
32451 TTTTAACACA ATTCTTCTCG TATTTGATAG GTCAAGCAGA GAAAACTTT
32501 AGTGAAGACA AAAACTTCTA AATACATAAG CTTGATTTAA TGGGCATGTA
32551 ATAGGACCTA GCATCAAAAA ATTAGAAAAA ATATTTTTTC TTAGGTATTT
32601 ATGGAACATG TATAAAATTT GATTTTCGTAG TAGGCCATAA AGCCAGGTTT
32651 AACACATTTT AAAGAACTGG TATCACAAGA ACTGCTTTCT CTGACCACTA
32701 TGCATTAAAA TAGAAGTTAA TTACAGACAT AAATTATAAA AATGCCAATA
32751 TTTTAAAGTG TGATATACAC TTCTCACTT ATGGGTCAAA GGAAATCGTA
32801 AGTGGAAATT CAAGGACACG TTGACTTGAA AACATTAATA CTTATGGAAT
32851 ATTTCTAAGA TGGAACCTGT ATGAATTTTA TAGTCTGAAA GCTTTTATTA
32901 GAAAAGAATT AAGTCTGAAA ATTAATGTGC TAAGTTAGGG GAGAGAAAAT
32951 GGAATAATCT CGAAGAAGGT AGGAGGAAGG AGATAATAAA GAATATATAG
33001 CAAAGATGCA GTAACAGGAT CAACAAAGCC AGAACTGTT GGAAAAGACA
33051 AGCCTCTGGA AAGATTGATG AAGAAAAAAG AGAAATGAGA TGTAATAATA
33101 TCATGTTTCA TTATAAATAG GCACATAAGG ACTTTTAAAA AACTAATAAA
33151 ATAATATGAA TCATTAATGC CAATAAATTT GAAAACAGAC AAAGTAGGTG
33201 AATTTCTAGA AAAATATAAC TTAAGTGGGAC TGAATGAAGA AGCAACAGCT
33251 TATAGTACCT AAGCAATTGA AGAGATTGGG TCAGTAATTT AAAATTTTCT
33301 CATAAACAAA ACGTTAGCCC CAGATGGTTC TTGCAAATGA TTAAAGAACA
33351 GATGTACAAA CATTTCCAGA GTGTAGAAGT AACTGTCTCT ATCCTTTCTA
33401 GGAGATCATT ATAACACCAA AAGCAGACAG TATATGAAAC AGGGAAATTA
33451 GAGGCCAAGA TACCTATGAC TTATATGTAA AAATTTAAAG AAAATATTAG
33501 CAACTGAAT CAGCCATTTT AAAAAATATA CCACAATCAA TGCATTCTA
33551 AGAGCAGCTT AACAAAATTT GTTAGAAGGC ATTAAGAAG ACTCAGTATA
33601 GAAAAGATGT ACCTTCTCTC CAAATTGGTG ATAGAGATTC AATGCCATTA
33651 AAAAAACCCA CCTGGTTTTT TTGAGGAAGT TGTCAAGCTG AGTCTCAAAT
33701 TTATATCAAA GAGCAAAGGC CTAAGAATAT CCAGGACATT CCTGAAGAAC
33751 TGTAAGGAGC CAGGGGCCTG CCCTATCAGA TACCAAGGGT TGTTATTAAG
33801 CCATAACCAA GTCAGTGCTG TTTCTACAGA AACAGACAAG TTAACAAGTG
33851 AAACATAATA GAGAGCCCAG AAACAGACCC ATCCATATTT TGGATTTGTC
33901 ACGTGAAAGA AGTAGCTTTG CAAAACTTTG GGAAAAGGAG AGTGTGTGCA
33951 ATAGATGATG CTCGTGCTCA TGCAGACAAA AAGGAAATTG GGATACCTGC
34001 CTCTTACCGT ACACAAACAC CAACCTAAAC GTGAAAGTTA AACTATAACA
34051 GCTTGAGGTG GTGGGAAGA AATATCTTTA TCTCAGTGTA GGAAGAATT
34101 TATTTTAAAA AGAAGACACA AAAGGCCATA CATAGGAATG AAAAGATTGA
34151 ATTCAGCTGC ATTAATAAGA TTAATTCAG CTGCGTTAAA ATCAAGAGCA
34201 TCTGTACTTG GACAGCATAG AGTGGAAAGA CAAAGAGAAG GTATTTGCCA
34251 GCTTATAACT TGAAGGATTA GAATGAATGA TATAAAGAAC TATGTAAATA
34301 AGAAAAAGAC ATACAACCGG TTAGAAAAAC GGGCAAAGAC ATGAACAGCA
34351 TATTTACCGT GAAGGAAACA GCGGTAGCAA ATGAACATGG TAAGAGATGC
34401 TCAACACGTT TAGTAATTTG AAGGGAATG CAAGTTATAC CCACAGCAAG
34451 ACTATCTTAT CTAGGAAGTT TGTCATACC CTAAATGTTT TGTGGTTTTA
34501 AGCTACAGAG TTTGTAATTC ATTTATTTAT TCAATAAATA CTCAGTGGCA
34551 GGCATGCTTT TGAAACCTT GGTATAACT TTGAATGAAA TTAACAAAAA
34601 TCTTGCCTT GTGGAGGATG CTTATGTGTG GGGAGTTGGG TGGTGGGGTC
34651 AAACAACAAT TACATTAATA TAGAAAAATG TGACATAAAT AAACCTATAA
34701 ATATTGCAAC CCAGAGTTAT ATTATAAATG TAAGTAGTGA CTAGGACTCT
34751 CATGCAGATA TACCTCTGTG CTGGGACAAA TGAAAGTTTA AGTGTAAATT

FIGURE 3-12



34801 CCCATATGCA AGTCAAAATA AAAAGTGACA CTAGAAAACA CAATAATGAA
34851 TATCTGAAAA TTGCATTTTA TTTGACTGCC ATCCTTTTGC ATCATTTTCA
34901 TACTAATTAT AGAATAAAAT TTGTAGGATG CACCAAAGCT TTTTITAGAG
34951 ACATCCATTA ATTCAATAAA TAAATGAGCA CCTTCTTTGT GCCAGCAGCT
35001 GTAAGAGGTG GCCCAAGGAA GGAATAAAAA CAGTCAAAAT CCTGGTACAC
35051 TCAGAGTTTC TCTTAGGAGA AAACAGATAC AAATGGCATT AATTACCAAG
35101 AAACCTTGTA AACAAGCCAA ATATTAATGA TAAATATTTG AGTACAGTAT
35151 GTTAATTTTA AGATTGAAAA TGAGGTGCCA GGATTTCTTA AGACTCAAAG
35201 GCGAAGATGG CTGAATAGGA ACAGCTCTGG TCTACAGCTC CCAGCGTGAG
35251 CGACGCAGAA GACGCATGAT TGCTGCATTT CCATCTGAGG TACCGGGTTC
35301 ATCTCACTAG GGAGTGCCAG ACAGTGGGCG CAGGTCACTG GGTGTGTGCA
35351 CCGTGCGCGA GCTGAAGCAG GGCGAGGCAT TGCCTCACTC GGAAGTGCA
35401 AGGGGTTCAG GAGTTCCCTT TCCTAGTCAA AGAAAGGGGT GACAGATGGC
35451 ACCTGAAAAA TCGGGTCACT CCCACCTGAA TACTGCACTT TTCTGACGGG
35501 CTTAAAAAAT GGCGCACCAG GAGATTATAT CCTGCACCTG GCTCGGAGGG
35551 TCCTACACCC ACGGAGTCTC GCTGATTGCT AGCACAGCAG TCTGAGATCA
35601 AACTGCAAGG CGGCGGCGAG GCTGGGGGAG GGGCACCCGC CATTGCCCAG
35651 GCTTGCTTAG GTAAACAAAG CAGCCGGGAA GCTCAAAATG GGTGGAGCCC
35701 ACCACAGCTC AAGGAGGCCT GCCTGCCTCT GTAGGCTCCA CCTCTGGGGG
35751 CAGGGCACAG ACAAAACAAA AGACAGCAGT AACCTCTGCA GACTTAAATG
35801 TCCCTGTCTG ACAGCTTTGA AGAGAGCAGT GGTTCTCCCA GCACGCAGCT
35851 GGAGATCTGA GAACGGGCAG ACTGCCTCCT CAAGTGGGTC CCTGACCCCT
35901 GACGCCCCGAG CAGCCTAACT GGGAGGCACC CCCCAGCAGG GGCACACTGA
35951 CACCTCACAC AGCCGGTTAC TCCAACAGAC CTGCAGCTGA GGGTCCTGTC
36001 TGTTAGAAGG AAAACTAACA AACAGAAAGG ACATCCACAC CAAAAACCCA
36051 TCTGTACATC ACCATCATCA AAGACCAAAA GTAGATAAAA CCACAAAGAT
36101 GGGGAAAAAA CAGAGCAGAA AACTTGAAAA CTCTAAAAAG CAGAGTGCCT
36151 CTCCTCTCCT AAAGGAACGC TGTTCTCAC CAGCAACGGA ACAAAGCTGG
36201 ATGGAGAATG ACTCTGACGA GCTGAGAGAA GGCTTCAGAC GATCAAATTA
36251 TCTGTAGCTA TTGGGAGACA TTCAAACCAA AGGCAAAGAA GTTGAAAACT
36301 TTGAAAAAAA TGTAGAAGAA TGTATAACTA GAATAACCAA TACAGAGAAG
36351 TGCTTAAAGG AGCTGATGGA GCTGAAAACC AAGGCTCGAG AACTACATGA
36401 AGAATGCAGA AGCCTCAGGA GCTGATGCGA TCAACTGGAA GAAAGGTAT
36451 CAGCGATGGA AGATGAAATG AATGAAATGA AGCGAGAAGG GAAGTTTAGA
36501 GAAAAAAGAA TAAAAAGAAA CGAGCAAAGC CTCCAAGAAA TATGGGACTA
36551 TGTGAAAAAG CCAAATCTAT GTCTGATTGG TGTACCTGAA AGTGACGGGG
36601 AGAATGGAAC CAAGTTGGAA AACACTCTGC AGGATATTAT CCAGGAGAAC
36651 TTCCCCAATC TAGCAAGGCA GGCCAACATT CAGATTCAAG AAATACAGAG
36701 AACGCCACAA AGATACTCCT TGAGAAGAGC AACTCCAAGA CACATAATTG
36751 TCAGATTAC CAAAGTTGAA ATGAAGGAAA AAATGTTAAG GGCAGCCAGA
36801 GAGAAAGGTC GGGTTACCCT CAAATGGAAG CCCATCAGAC TAACAGCGGA
36851 TCTCTTGCCA GAAACTCTAC AAACCAGAAG AGAGTGGGGG CCAATATTCA
36901 ACATTCTTAA AGAAAAAGAT TTTCACCCA GAATTTTATA TCCAGCCAAA
36951 CTAAGCTTCA TAAGTGAAGG AGAAATAAAA TCCTTTACAG ACAAGCAAAT
37001 GCTGAGAGAT TTTGTACCA CCAGGCCTGC CCTAAAAGAG TTCCTGAAGG
37051 AAGTGCTTAA CTTGGAAAGG AACAATCAGT ACCAGCCGCT GCAAATCAT
37101 GCCAAAATGT AAAGACCGTC GAGACTAGGA AGAAACTGCA TTAACAAACG
37151 AGCAAAATAA CCAGCTAACA TCATAATGAC AGGATCAAAT TCACACATAA
37201 CAATATTAAC TTTAAATGTA AATGGACTAA ATGCTCCAAT TGAAAGACAC
37251 AGACTGGCAA ATTGGATACA GAGTCAAGAC CCATCAGTGT GCTGTATTAA
37301 GGAAACCCAT CTCACATGTA GAGACACACA TAGGCTCAAA ATAAAAGGAT
37351 GGAGGAAGAT CTACCAAGCA AATGGAAAAA AAAAAAGAC AGGGGTGCA
37401 ATCCTAGTCT CTGATAAAAC AGACTTTAAA CCAACAAAGA TCAGAAGAGA
37451 CAAAGAAGGC CATTACATAA TGGTAAAGGG ATCAATTCAA CAAGAAGAGC
37501 TAACTATCCT AAATATATAT GCACCCAATA CAGGAGCACC CAGATTATA
37551 AAGCAAGTCC TGAGTGACCT ACAAAGAGAC TTAAACTCCC ACACATTAAT
37601 AATGGGAGAC TTTCACACCC CACTGTCAAC ATTAGACAGA CCAATGAGAC
37651 AGAAAGTCAA CAAGGATACC CAGGAATTGA ACTCAGCTCT GCACCAAGCA

FIGURE 3-13

37701 GACCTAATAC ACATCTACAG AACTCTGCAC CCCAAATCAA CAGAATATAC
37751 ATTTTTTTC A GCACCACACC ACGGCTATTC CAAAATTGAC CACATACTTG
37801 GAAGTAAAGC ACTCCTCACC AAATGTAAAA GAACAGAAAT TATAGCAAAC
37851 TATCTCTCAG ACCACAGTGC AATCAAAC TA GAACTCAGGA TTAAGAATCT
37901 CACTCAAAAC CGCTCAACTA CATGGAAACT GAACAACCTG CTCCTGAATG
37951 ACTACTGGGT ACATAACGAA ATGAAGGCAG AAATAAAGAC GCTCTTTGAA
38001 ACCAACAAGA ACAAAGACAC AACATACCAG AATCTCTGGG ACGCATTCAA
38051 AGCAGTGTGT AGAGGGAAAT TTATAGCACT AAATGCCAC AAGAGAAAGC
38101 AGGAAAGATC CAAAATTGAC ACCCTAACAT CACAATTAAA AGAACTAGAA
38151 AAGCAAGAGC AAACACATTC AAAAGCTAGC AGAAGGCAAG AAATAACTAA
38201 AATCAGAGCA GAACTGAAGG AAATAGAGAC ACAAAAAACC CTTCAAAAAA
38251 TTAATGAATC CAGGAGCTGG TTGTTTTTGA AAGGATCAAC AAAATTGATA
38301 GACCGCTAGC AAGACTAATA AAGAAAAAAA GAGAGAAGAA TCAAATAGAC
38351 ACAATAAAAA ATGATAAAGG GGATATCACC ACCAATCCCA CAGAAATACA
38401 AACTACCATC AGAGAATACT ACAAACACCT CTATGCAAAT AAAGTAGAAA
38451 ATCTAGAAGA AATGGATAAA TTCCTCGACA CATAACCCCT CCCAAGACTA
38501 AACCAGGAAG AAGTTGAATT TCTGAATAGA CCAATAACAG GATCTGAAAT
38551 TGTGGCAATA ATCAATAGCT TACCAACCAA AAAGAGTCCA GGACCAGATG
38601 GATTACACAGC CGAATTCTAC CAGAGGTACA AGGAGGAACT GGTACCATTG
38651 CTTCTGAAAC TATTCCAATC AATAGAAAAA GAGGGAATCC TCCCTAACTC
38701 ATTTTATGAG GCCAGCATCA TCCTGATACC AAAGCCAGGC AGAGACACAA
38751 CAAAAAAGA GAATTTTGA CCAATATCCT TGATGAACAT TGATGCAAAA
38801 ATCCTCAATA AAATACTGGC AAAGTGAATC CAGCAGCACA TCAAAAAGCT
38851 TATCCACCAT GATCAAGTGG GCTTCATCCC TGGGATGCAA GGCTGGTTCA
38901 ATATACGCAA ATCAGTAAAT GTAAATCCAGC ATATAAACAG AACCAAAGAC
38951 AAAAACCA CA TGATTATCTC AATAGATGCA GAAAAAGCCT TTGACAAAAT
39001 TCAACAACAC TTCATGCTAA AAAGTTTCAA TAAATTAGGT ATTGATGGGA
39051 TGTATCTCAA AATAATAACA GCTATCTATG ACAAACCCAC AGCCAATATC
39101 ATACTGACTG GGTAAAAACT GGAAGCATTG CCTTTGAAAA CTGGCACAAG
39151 ACAGGGATGC CCTCTCTCAC CACTCCTATT CGACATAGTG TTGGAAGTTC
39201 TGGCCAGGCG CCTTAGGCAG GAGAAGGAAA TAAAGGGTAT TCAATTAGGA
39251 AAAGAGGAAG TCAAATTGTC CCTGTTTGCA GACGACATGA TTGTATATCT
39301 AGAAAACCCC ATTGTCTCAG CCCAAAATCT CCTTAAGCTG ATAAGCAACT
39351 TCAGCAAAGT CTCAGGATAC AAAATCAATG TACAAAAATC ACAAGCATTG
39401 TTATACACCA GCAACAGACA GAGAGCCAAA TCATGAGTGA ACTCCCGTTC
39451 ACAATTGCTA CAAAGAGAAT AAAATACCTA GGAATCCAAC TTACAAGGGA
39501 TGTGAAGGAC CTCTTCAAGG AGAACTGCAA ACCACTGCTT AATGAAATAA
39551 AAGAGGATAC AAACAAATGG AAGAACATTC CATGCTCATG GGTAGGAAGA
39601 ATCAGTATCG TGAAAATGGC CATACTGCCC AAGGCAATTT ACAGATTCAA
39651 TGCCATCCCC ATCAAGCTAC CAATGACTTT CTTACAGAA TTGGAAAAAA
39701 CTACTTTAAA GTTCATATGG AACCAAAAAA GAGCCCGCAT TGCCAAGTCA
39751 ATCCTAAGCC AAAAGAACA AGCTGGAGGC ATCATGCTAC CTGACTTCAA
39801 ACTATACTAC AAGGCTACAG TAACCAAACC AGCATGGTAC TGGTACCAAA
39851 ACAGAGATAT AGACCAATGG AACAGAACAG AGCCCTCAGA AATAACGCCG
39901 CACATCTACA ACTATCTGAT CTTTGACAAA CCTGAGAAAA ACAAGCAATG
39951 GGGAAAGGAT TCCCTATTTA ATAAATGGTG CTGGGAAAAA TGGCTAGCCA
40001 TATGTAGAAA GCTGAAACTG GATCCCTTCC TTACACCTTA TACAAAAATC
40051 AATTCAAGAT GGATTAAAGA CTTAAACGTT AGACCTAAAA CCATAAAACC
40101 CCTAGAAGAA AACCTAGGCA TTACCATTTA GGACATAGGC ATGGGCAAGG
40151 ACTTCATGTC TAAAACACCA AAAGCAATGG CAACAAAAGC CAAAATTGAC
40201 AAATGGGATC TAATTAAACT AAAGAGCTTC TGCACAGCAA AAGAACTAC
40251 TATCAGAGTG AACAGGCAAC CTCCAAAATG GGAGAAAATT TTTGCAACCT
40301 ACTCATCTGA CAAAGGGCTA ATATCCAGAA TCTACAATGA ACTCAAACAA
40351 ATTTACAAGA AAAAAACAA ACAACCTAT CAAAAAGTGG GTGAAGGACA
40401 TGAACAGACA CTTCTCGAAA GAAGACATTT ATGCAGCCAA AAAACACATG
40451 AAAAAATGCT CACCATCACT GGCCATCAGA GAAATGCAAA TCAAAACCAC
40501 AATGAGATAC CATCTCACAC CAGTTAGAAT GGCAATCATT AAAAAGTCAG
40551 GAAACAACAG GTGCTGGAGA GGATGTGGAG AAATAGGAAC ACTTTTACAC

FIGURE 3-14



40601 TGTGTGGTGGG ACTGTAAACT AGTTCAACCC TTGTGGAAGT CAGTGTGGCA
40651 ATTCCTCAGG GATCTAGAAC TAGAAATATC ATTTGACCCA GCCATCCCAT
40701 TACTGGGTAT ATACCCAAAG GACTATAAAT CATGCTGCTA TAAAGACACA
40751 TGCACATGTA TGTTTATTGT GGCACTATTC ACAATAGCAA AGACTTGGAA
40801 CCAAGCCAAA TGTCCAACAA TGATAGACTG GATTAAGAAA ATGTGGCACA
40851 TTTACACCAT GGAATACTAT GCAGCCATAA AAGATGAGTT CATGCTTTTT
40901 GTAGGGACAT GGATGAAATT GGAAATCATC ATTCTCAGTA AACTATCACA
40951 AGAACAAAAA ACCAAACACC GCATATTCTC ACTCATAGGT GGGAATTGAA
41001 CAGTGAGAAC ACATGGACAC AGGAAGGGGA ACATCACACT CTGGGGACTG
41051 TTGTGGGGTG GGGGGAGGGG GAGGGATGGC ATTGGGAGAT ATACCTAATG
41101 CTAGATGACG AGTTAGTGGG TGCAGCGCAC CAGCAAGGCA CATGTATACA
41151 TATGTAACTA ACCTGCACAT TGTGCACATG TACCCTAAAA CTTAAAGTAT
41201 AATAATAAAA AAAAAAGACT CAAAGGCACA GTCAC TGACA GTTTGATTTT
41251 TTATAATAGC TGTTAATTTT CCTAACTTCG AGGAAGTTGA TAGCATGTTT
41301 TGAGTATATT TCAAAACTAC ATTCAAATGT TGCAATAGAA CATTAAGAAT
41351 TATCTTCATG ATCCACTAAG TGCATGAAAA AAATGGATAA TGAATCTATT
41401 CATTACCATC GTTTAATATT TTATCTTCAA GTTTTTGTGT TTTGTAGCTC
41451 ATTGGCAGAG TTTGACAGAG TGCTGAAAGT ATTCTTTAGT GAGCTGGCTG
41501 TAATTTTTTG GCGCATTTTT ATCTAGATAA TTAAAACTAT CTGACAGGAC
41551 CATAAAATGC TTGCTGCCAT TTCCAACAAC CTATATTTGT GGATGGGGTT
41601 TTTTAATTTA ATGAGAATAT TATGTTAGAA AAGAAACTGT CATTCTGTAA
41651 AGTGGCCAAT AATGTTAGTT TTATTTATCA ATTTAGTTTT GTACTTTGAT
41701 CATTTTTTTA AAATTTTCAGC ATTGATGTTG ATGGGACAAT GACAGTGGAC
41751 TGGAAATGAAT GGAGAGACTA CTTCTTATTT AATCCTGTTA CAGACATTGA
41801 GGAAATTATC CGTTTCTGGA AACATTCTAC AGTAAGTCTA CTTTATGTAT
41851 TTATACTTAT TTGGAGCTAT AAACCATAGG TACAGTTATC ACCCAAGAAC
41901 ACTCTGTAAC ACTTATGGGC CAGGATACCT GAGTCCAGT AGCTCCTTAA
41951 CCTGTAGAGT TCTATTTATT CTATTAGGCA TAGATTTATA GAGTATTAAA
42001 CAAAAAAGAG CAGCTCTCCC TCTCCCTCTC CCTCTCTCTC CCCCTCCCCA
42051 CGGTCTCCCT CTCCCTCTCT TTCCACGGTC TCCCTCTGAT GCCGAGCCAA
42101 AGCTGGACTG TACTGCTGCC ATCTCGGCTC ACTGCAACCT CCCTGCCTGA
42151 TTCTCCTGCC TCAGCCTGCC GAGTGCCTGC GATTGCAGGC GCGCACCGCC
42201 ACGCCTGACT GTTTTTCGTA TTTTTTTGGT GGAGACGGGG TTTCGCTATG
42251 TTGGCCGGGC TGGTCTCCAG CTCCTGACCG CGAGTGATCC ACCAGCCTCG
42301 GCCTCCCGAG GTGCTGGGAT TGCAGACGGA GTCTCGTTCA CTCAGTGCTC
42351 AATGGTGCCC AGGCTGGGGT GCAGTGGCAT GATCTCGGCT CGCTACAACC
42401 TCCACCTCCC AGCCGCCTGC CTTGGCCTCC CAAAGTGCCA AGATTGCAGC
42451 CTCTGCCCAG CCGCCACCCC GTCTGGGAAG TGAGGAGCGT CTCTGCCTGG
42501 CCGCCCATCG TCTGGGATAT GAGGAGCCCC TCTGCCTGGC TGCCCAGTCT
42551 GGAAAGTGAG GAGTGTCTCT GCCCGGCCGC CATCCTGTCT AGGAAGTGAG
42601 CGTCTCTGCC CGGCCGCCCA TCGTCTGGGA TGTGAGGAGC CCCTCTGCCT
42651 GGCTGCCCAG TCTGGAAGT GAGGAGCGCC TCTTCCCGAG CGCCATCCCA
42701 TCTAGGAAGT GAGGAGCGTC TCTGCCCGGC CGCCATCGT CTGAGATGTG
42751 GGGAGCGCCT CTGCCCGGCC GCGCCGTCTG GGATGTGAGG AGCGCCTCTG
42801 CTCGGCCGCC CCGTCTGAGA AGTGAGGAGA CCCTCCGCCC GGCAGCCGCC
42851 CCGTCTGGGA AGTGAGGAGC GTCTCCGCCC GGCAGCCACC CTGTCCGGGA
42901 GGGAGGTGGA GGGGTGAGCC CCCC GCCCGG CCAGCCACCC CATCCGGGAG
42951 GTGAGGGGTG CCTCTGCCCG GCCGCCCTA CAGGGAAGTG AGGAGCCCCT
43001 CTGCCCGGCC ACCACCCCAT CTGGGAGGTG TACCCAACAG CTCATTGAGA
43051 ACGGGCCATG ATGACAATGG CGGTTTTGTG GAATAGAAAA AGGGGAGAGG
43101 TGGGGAAAAG ATTGAGAAAT CGGATGGTTG CTGTGTCTGT GTAGAAAGAG
43151 GTAGACATGG GAGACTTTTC ATTTTGTCT GTACTAAGAA AAATCTTCT
43201 GCCTTGGGAT CCGTGTGATC TATGACCTTA CCCCCAACC GTGTCTCTCT
43251 GAAACATGTG CTGTGTCCAC TCAGGGTTAA ATGGATTAAAG GGCGGTGCAA
43301 GATGTGCTTT GCTAAACAGA TGCTTGAAGG CAGCAGGCTC GTTAAGAGTC
43351 ATCACCCTC CTAATCTCA AGTACCCAGG GACACAAACA CTGCGGAAGG
43401 CCGCAGGGTC CTCTGCCTAG GAAAACCAGA GACCTTTGTT CACTTGTTTA
43451 TCTGCTGACC TTCCCTCCAC TATTGTCTG TGACCCTGCC AAATCCCCCT

FIGURE 3-15

43501 CTGCGAGAAA CACCCAAGAA TGATCAATTA AAAAAAAAAA AAAAAAACA
 43551 ACCCAAGACT GCATAAATGT CCATTCTGAA AACTTGGAAG AAGTACCACC
 43601 TTGATGAATA AGCTGTCTAG CTTTTATTGG CATTTAAGTA TTCTGCCATA
 43651 GGGAAAGTGTA AAAGTTGTAG GCTTTTACTT TTTATAGTA CTATATTGTC
 43701 CAAATAATCT CAGCACCTCA TGGTTGCTAA GGATCTGTGT CCTTGTTTGG
 43751 TCAGATTATG TTTATCTCTG GCATAAGGCA CTTAACAATA TTCATTAAAG
 43801 GTTACAGAAT CTTTTTGCTT CATCTGCTTA GCATTTTCATA CCAGTTTGTT
 43851 TTCCACCAAA CTTTCAAATT TTGATTGTTT CATTAATATT CTGCATACTG
 43901 ATGTAAACCA AGTTCTATTA TTGTGCAATC TGCTCCTGAA ACCCTTAGGA
 43951 ACTCTCTGAA GGAGTTTTAT TTATTTTTTG TTTTGTGTTT TGTTTTTGTT
 44001 TTGTTTTTTT GAGACGGAGT CTTGCTCTGT TGCCCAGGCT AGAGTGCAGT
 44051 GGTGCGATCT CGGCTCTCTG CAAACTCGGC CTCCGGGGTT CAGGCCATTC
 44101 TCCTGCCTCA GCCACCGGAG TAGCTGGGAC TACAGGCACC CACCACTGCG
 44151 CCTGGCTAAT TTTTTTGTA TTTTATAGTAG AGACGGGGTT TCACCGTGTT
 44201 AGCCAGGATG GTCTCGATCT CCTGACCTTG TAATCCGCCC GCCTCGCCTC
 44251 CCAAAGTGCT GGGATTACAG GCGTGAGCCA CTGTGCCCGG CCTTTTTTTT
 44301 TTTTTTTCT TTAGGGCTT GTCTTCTACA CTTCAGATTT GACTAAATTA
 44351 AATAGTCATT AAATGAAGTC AGGAGTTCAC ATTGCCACTA GTAACAATGC
 44401 CTAAGCTTAC ATAAAGCATT ATAAAATTGT TGGTGATTAG TGCCTTCTCA
 44451 GCTATGAGTA TAAGATAATA TTATACTAGT AGTTCAGTTG CCTAGATAAA
 44501 TTGTACACTA TGTGAAGTTT TATTTACATA ATTCTTACGG TATTTTTTAA
 44551 GGTAGTTGAT AACAGTTGAG ACTACAATTG TATCTCCATT TTATTGATAG
 44601 TAAAATGAAG GAAGGGAGGG TTAATACTCAT AGGAGAGCTC CTCCCCGTTG
 44651 CACTCTTGCC TGTAAAAATT TTTCTGCCAA AACAATTTAG ATAATAGAAT
 44701 TGTAAAAATA TTATTATAGA ATTGTTTCTC TCAAACATA GTAATGTAGA
 44751 ATAGGTTGAA GGGGTGATGA TTTGAAACAA TACCTCTCCA TTAGCTAAAT
 44801 TTTATATAGA ATCTATTGCA TGTTTTAAAT GATAAGTCAG ATTTATAAAA
 44851 ATATTTTTAT AAACAGTAGG AAATGAGTTT AGGGGTATTC ACATACAGTT
 44901 TTAATTTTTA TTTACATATT TAAAAACAT CATGGTATAA ATATGATGTG
 44951 GATATAAATT TGAGATAAAG GAAGTATTGT TTAAGAATTG ATGAACATAT
 45001 TTCTTAAAG ATGTCATCAC CAGTTGGTTT TCTAGCCTTA TGAAAAATGG
 45051 TTGCAATAAA AAAGATTGAC TATGATAAAA TGCTGCCCTT TCATTTTAAC
 45101 CTAGACCAAG AGAAAACATA CTGTGAATCT ATGATGAATG AAAGAAAGTT
 45151 GTAAGTGTG GTTTTGATA TTTGTAATTA CTGTTTATTT TCATTTCTTG
 45201 TGAAGTATA CTGTACTTTG TTCATTGTGA GTAGACAACT TATAATCTAT
 45251 GTAAGTATA TGGTTTAGTA TAAATTCTAG GGAATGAAGT TCATATTAAC
 45301 TGTAAAAATA CATGATTGTT CTCTAAAACA AAACGTCTTC TGGGATTATT
 45351 TTTAACTAAG GCGCATGGGG ATCTTTTTTT CATTTTTACA GGAATTGAC
 45401 ATAGGGGATA GCTTAACTAT TCCAGATGAA TTCACGGAAG ACGAAAAAAA
 45451 ATCCGGACAA TGGTGGAGGC AGCTTTTGGC AGGAGGCATT GCTGGTGCTG
 45501 TCTCTCGAAC AAGCACTGCC CCTTTGGACC GTCTGAAAAT CATGATGCAG
 45551 GTGAGCTTTA TTATCGTGTG TCCAGGTTTG CCCTAAATAT TCTAAAACAA
 45601 TGAGAAATGT GGTGCTTTGA AAAAGAAGTT TTAAAATTTT TCAGTAATAA
 45651 TCTTTTATAC CCTAAAAAAT AAATCTATTT TGTTGCTGTT AACTCTAAAT
 45701 TCAGTCCATG TAAGTATGGC AGTGTACCAA ACCTTAAATT GTTAGTACAT
 45751 GTGTGTAATG AACTTTTAAT CTTTGGCATT CTATGACTAT TCAAACATTT
 45801 AATTCAAAAA ATATCTCTAG CTATTGTTGT AGGATTCTCC TGATTTATAG
 45851 TTTCTTCTTT TTTAATATAC TTTATCAAAA GTAAAGTATT TTTGAAATCT
 45901 AGACTCTTAG AGCAGCAATG TAATTTTGAA AATTATTCTA AAGCTGAGGT
 45951 TAGCAGAAAA AGATCTGGCT TTATAGACTG ACTTTGCTAT TTAGTAGCAG
 46001 TGTAGCATTG GGCTGGCCAG AGTGGAAGA GGAATGGAA AAGAATTAAT
 46051 ATGTATTTGC TCACTGTGGT AACCCAGTTA ATCCTTGCAAG CAGCCAGTG
 46101 AAGTAGGATG TTTATCATTT TTCCAGGGGG AATCTGAGGC CCAGAGAATT
 46151 GACTTTTCTT TTACAACAAA TGAGAGGGGG AATGCAGTAT CTTTGCCCTC
 46201 AGTGCTCCTG GTTCTCATGC TGCAAGAAAC CTCTGAGGTC TCATTTTCTT
 46251 TCATTCTGGG ATGGGGATAA GAATATCTAA TAAGAATGGT TTAAGAATCA
 46301 AGCAATATCA GGTATGTGAT AATGTCTGGT ACACTGGAAT AACCTATTGG
 46351 AACATAGTAG TTGTTTACAA AATATTTTAA AAACCTTGTT ATACTTATGG

FIGURE 3-16

46401 TCAACACTTT TTATATTTGT CTGTAGATTT CTGTACAAAA AGATTCTGAC
46451 ACTGTTTTAA GCCAGCATT CTTCAGAATG TACCCAAATC TCAAAATTTA
46501 TTTAGGGGCA AAGCTAATGC TTTAAAGAAA AAGGAGAGGG GATTGGTGTG
46551 TGTTTTTCTT TAGGAACAGT AGTAACTTGA CTTTATAGAGA ACTTGAATAA
46601 GCATTTATTT TTTCTTTTGT CCTATTTTAT TGTGAAGTTT ATTTATTTAA
46651 AATAAAATGG ATTTCTCTGG AATTTAGTTT CTGCAAATTT GAGGAGTTTC
46701 CAAAGTCAAC CTTCAGGTTT GATACTTCTC TAGAAAAGACT CACATAACTC
46751 ACTGAAAGCT TATTACCCCT GGTATGTTT TATTACGGGG AAAAGATGCG
46801 GATGAAATC AGTCAAGTAA AGAAGCACAT AGGGCAGAGC TTCTGTTGTC
46851 CTCTCCCTGT GGAGTCTCCA TGTCTTACTT TCCTGGCACT GTTATGTGGC
46901 ACTAGGCATG GAATATTGCA GACCAACCAG GGAAGCTCAC CTGAGCCTTT
46951 GGTGTGCAGA GTTCTTATTG GGGCCTGTTT TCATACTGGC CACATGGCTG
47001 GCCTTCAGAA TTCAACCCGT TCTGTGAGTG TGTGTGTGTG TGTGTGTGTG
47051 TGTGTGTGTG TGTTTAGTGG TAGTCACCCC TTTTATGTGA GCTGAAACAA
47101 TCAGAAGAAT AGCTGATTTG TTTAATTATT TTTGGTGTAT TGGACTTAAT
47151 CAGTTTTTAT CTGTAGGTGG TCATAAGGTA CAGTATTTTT AAGTGACTAC
47201 CACATCTGTA GTATAAGCCA AGTAATTTAT CAGTACTCAC AGGATGGGTA
47251 CATGTTGTAA TGAATTTATT GCCTAGAGAG GGCCTCAAAA TATGCCAAG
47301 AGGGTGCAAT TTTTATTTTT GGTTTCAGGC TGTATGCATT CCAGTGTGG
47351 TAGCCCTGAT ATACACAATA TCCAAACCAT TTCAGACCCA TTTACAGTTC
47401 ATGTCTGTAC TACTTCTTGA GGAGAGGGAG TAACATATTA CTTTAAATTA
47451 TATGTAATAA TATACATACA TTAAATTATA TGTAATAATA TAATATTATT
47501 ATTTGCAGTA TACTTTTTTA TTTCCCTTTA ACTGAGCTTG TTCATGTTTC
47551 AAAGGGTGTT CCATTGCCTG ATACATAATT TAGTTAATAT TATCTTATGA
47601 AGGTTGTTCA TAATTTTAAT ACTCTTCTTG TCTTCTCTCT CTGCTTTCTC
47651 ACACTGAAGA TACCAATTAT TCTTAGTTTT AGAGTCAGAG ACAGGCCTCT
47701 AAAATCATGG CAATACTCCC TCTCATCATT ATATATATTT TTCAACCTTT
47751 CTATATTTTA TTTTCAAATA TATCTTCTTG CAGTTAGAAA CGGTATTGAA
47801 AAAGATTGTG TGGTTGTTCT AGAAAAAGTA ATAGTAATAT GCCACCAGCA
47851 TTTTATATCA TTCCTTTTTT ATTTTATAGT TCACGGTTCA AAATCAGACA
47901 AAATGAACAT ATTTGGTGGC TTTTCGACAGA TGGTAAAAGA AGGAGGTATC
47951 CGCTCGCTTT GGAGGGGAAA TGGTACAAAC GTCATCAAAA TTGCTCCTGA
48001 GACAGCTGTT AAATTCTGGG CATATGAACA GGTAATTGTT ATCACCCGTG
48051 GAATTTATTA ACAAAGAGGA GTTAGTAAAC GGATTCAATA AATGTTAATG
48101 TATAATGCTT TTGGGATTCT TGTTTTAATA CATGATAATC TTTCACATAT
48151 ACCCCATAAG GAGGATCACT TATAGGAGAT TAGACTAAAT AAAATCAGAG
48201 ATTTCTCATG ACCAAGTTAT GGGATTCTTA ATTCATCATA TTATTTATAA
48251 AGTTTTTTTT TTCTAAGTAG TTCTTAAAGG AAGGGTAGAA TTTTAGTTTA
48301 TTCATTCTGA ATCCTGAGCA GAAGCAGCAC ACTAACATAA GTTTTATGAA
48351 AGTGTACAAA TCTAACCTCT GGAAGGAAAA CTATAAGTTG AAGTCCTTTG
48401 TGTAATTTGA CGTTGCTGTA AAATTGAGCT GAGTTTGGAG TGACACCTCC
48451 ATGAAGGCAG GGGCGTGGCT TCTTCCCAT GTACTCCAGC ACCTAGACAG
48501 AGCTTGGCAT GTGATAAGTT TCAAGCGAGT GTTGAATGAG TCAATGAATG
48551 AACAAATGCA TTTACCTCTG AATCACTTCT CTGTCGGCTT TTGTAACTT
48601 GGATTATTTG AGCTATTGCT TCAGCCTAAC TCAATGTAAA GGGGAAATAC
48651 AGAGGTAAGT TTTAGAGTTT GGGTTCTCTT TATGGTCATT AGCAGAACTG
48701 TCTAGTTGAG CAGCCACAGA TTATGTTTTT CATTATTTAT TCCATCATTG
48751 TTTATCAAGG ACTGTAAGGG CCTTGAAATT CAACTCCCCC CCCCATAGTT
48801 TTTGTATTAT TCCATGTAGA TTTTAGATTA TTCTGGAGAG TGTTTTGTTC
48851 TTGAGCAACA GAATACTCTT GAGAAGATTA CGAAGTCCAG TGGTATCCTT
48901 TTCTTTGCCT AGGAAATAGA GAAGCAAAAA AAAAAAAAAA AAAAAATTAA
48951 AGAAAAATCTA GTCTCCAGGA TTTTAATTAG AACCTATCCT TGGGAAGGCT
49001 ATTTTCCTTA TATGAAGGTT TGAAGATTCA AATCATGATT ATTAAGGGCT
49051 AATGTTTAG ATACCCTTAG GTTATTCTGA CCACATACTT GGATTTTATG
49101 ATAGGAAAGC CACAGCCTAA AATAAATAAA TACTCAATGC AGTTATTTCA
49151 GTATGCAAGA AGTTTGGTAT TTTTGAAAAA GTCCATGGGT ATTGCAAGCA
49201 AATATGCACA TTTTGCTTTA TGCCATTTGT CAGATTCTTA CCTTGATAC
49251 CACCAACAGG CATCCTCTGC TTCTGTCCAC CCAAGCTCCT TCCTGAGACC

FIGURE 3-17



49301 TCTTTATAGT ATTGTGATTT CTGCACACTA ACTTTCCTTAG ACATGAAGAG
49351 AAAGCTGTCT ACACAGTGTG GTGTAGTTTT CTATGGGCT CTGGACCTAT
49401 GGTGCTGTTT TCTCTCCTCC TGCTGAAGGT CCATTCATCC CTCGGGGCTC
49451 TCTAAAAGCC ACCTTCCTGT GACAAGCATA TACTAAGCAT CTCAATCAAA
49501 GCCAGTTCCT CCCCTGTCCA GCCTCCCTCG AGTGCTGAAT TGCAGAATAT
49551 CCCATTTTTT ATTGGATGAT GGAAAACCCA TTGTTTTCCC AGTGGATTGT
49601 AAATTACTTC GGGGTAAATA GGCTGTATAT ATTCTCAAAT TTCCCAGAGT
49651 ATGTAAGTAG GTCACTTTTA GATTCAGATA GATTTTGTTT CTTGAATAGC
49701 TAGTACTTTA GGAACTAAG AAAAAGATCT TTCAACCTG GTATGTAGCT
49751 CTGTCAAACA CATCATCAGT ATGGGGTAAA CCTGTGTTCT CTGTGGGTTG
49801 TCATTACCAT AGTAGTGTCA TTGTATCATT GACAGTGTA TAGTGTGGGG
49851 TAGTGTTCTT GTGGTTTCAG CTGCCACTCT GACTGACTG CTTTCCACTC
49901 CAACATCTTC CTCTTTATCT CAACACTGTA GGTCTACCTG TGTACTGTGT
49951 GTTTCAGCAT CTCTGCTTGC ATGACCCAGG AGTGCCTCCC ACTCAATATG
50001 GCCACCATGC ATGGTCATCT TTCTGCTACT CCCTGTCTCC TGACCCTGCT
50051 CCAGCAACAC AGACAGACAC CCTTCCTCTT TCTATATGTC ATATGGTGGG
50101 GAATGCCCTT TAGTACTTAC TCAGGAGTTA GTTCCTCTGG GAAGCCTTCT
50151 GTTCTAGTTT CCTTTTGTTA CAGCACTTTC ACATTGAATT CTGACGTTCT
50201 CTGTACTTAT CTGCTTTGTG AGACTGTGAG CTTCCCTTAGG CAGTAGCTAC
50251 TTGTATTCTT AGCACCTTGC CCAGTGCCAG GAAACCCCTTA TTAAGTAAAT
50301 GAAAAGACAG AACTGACAGA CTGGAATTAG AGCTCAAGCT TGCCTCAATC
50351 TCAAGCCATT AAGATGAAGG GGAGCCGGGC GTGGTGGCTC ACGCCTCTAA
50401 TCCCAGCACT TTAGGAGGTA GTTTGCTTGA GCCCAGGAGT TCAAGACCAG
50451 CCTGGGCAAC GTGGCAAAAC CCCATTTCTA CAAAAAATAT AAAAATTAGT
50501 TGGACGTGGG GGTGTGTGCC TGTAAGTCAAG ATGCTGAGGT GGGAGGATCA
50551 CTTGAGCTCG AGAGGCAGAG GTTGCAAGTA GCTGGGATCA CACCATTGCA
50601 ATCTAGCCTG GGTGATAGAA TGAGACCTTG TCTCAAAAAA AAAATAAATA
50651 AATAAATAAA GGGGAAGATA AGGATTGGAA ACAGAAGGAG CAGCATGTGG
50701 ACAGAAATGT AGGCACAAGA AGGCATCACT CACTGAAGAG ACTGAAAGTG
50751 GTTCACTGTG CCTCAAGACT GGTGGAGTGT GTTCCCGGAA AGATAATGAT
50801 GAAAGAGCTG CAGGATAAAA CAGGGGCCAA ATGTAATAGG AGTCTGGATT
50851 TTATTCTGAA TATGGTAGGG GCTATTGTAG CATCTTATAT AGGGAAGTGA
50901 AATGAGTACA TTCACATTTA AGGAATATCA ACCTGAAAAA AGAGTGGAGA
50951 CATTGTTGGG GGAGAGTGAG GTAGACTAGA GGCAGGGAGA ATATTTAAAT
51001 AATTGAGGTA AGAAATGATG AACACCAGTA TAAGGTGATG TCTTTAAGGA
51051 ATGGAGAAGG GAATGAAGT AGAAATATTT TGGAAGTAGA ATCAACAGAA
51101 CTCACCTGAT GACTGGATAT GGAGGTGAGA AAGAGAAGAG TCAAGAATGA
51151 TATTCTAATT TCTAACTTGA GTGACTGCAT TCAAAGAGAA TACAATATCA
51201 GGTTCCATTT TGTGCATGCT GAGTTTGAGA TGTGTGGGAC ATGTACAGGG
51251 AGCTGTCCAG TAAGCAATTG GGTATATCAG CTAGCCATTA AGAGAGAGAT
51301 CTTTGATAGA GAGGTTGTTG CTGAGTTGAG CCATTGGAAT GGGCAGGATC
51351 ACTCAAGAAG AGCTTATAAA TGAGAAGAAT TCTAGGAATA AGTCCAAAGG
51401 GAGAAGTAAA AGAAGAAACT TGCAAAGGAC ACTGAGAAGA AATAGCTCGA
51451 GGGATGGGAG AAAATCCAGA GAGAGGGATG GCATAGGAGT CAGTGGGAAGG
51501 AAACGGTTTC ATGGGGGTCA GTACTACTGG GTAGTGAATA TAATAAGAAT
51551 ATCTTTTAGG ATTTCTCAAC CCAGAGATAG GTAAGCTTAG TATAAATGCT
51601 TCTGTGAAGT AATGAAATGA GAAACCATGC TGAAATGAGC TTAAAGTGAA
51651 TGGGAGGTGA AGAACTTGG ACAGTAGAGA CACATTTTGA GGGAGTTTGA
51701 CAGTGAAGAG AAGGAACTA GAAGAGGGAG AGGGTGATAG ATAAGAAAGA
51751 TGTTGGGTGG AGGGGATTTG TTTTTTGT TTTTGT TTTTCTGTTT
51801 GTATGTTTGT TTGTTTTTGA GATGGAGTCT CACTTTATCA CCCAGGCTGG
51851 AGTAAAGTGG TGCAATCTCA TCTCACTGCA ACCTCTGCCT CCTAGGTTCA
51901 AGTGATTCTT CTGCCTCAAC CTCCTGAGTA GTTNNNNNNN NNNNNNNNNN
51951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
52001 NNNNNNNNNN NNNNNNNNNN NNNNNNTGCCT CAGCCTCCCG AAATGCTGGG
52051 ATTGCAGGAG TGAGCCCCC GTGCCTGGCC TGGAGGGAGG ATTTTGATTT
52101 GACTTTAATG TGCCTGTTGC TGAAGGAAGC ATGTCAATAC AAATAAAGAA
52151 GTTGAACA TAGGTAAGAG AGGTGATTA ACCCGGTAGG TGTTTCAAGG

FIGURE 3-18

52201 GAGTTTGTGT GTAGGGAAAG GGAGTGGGAG ATGGAAAGGG GCTGGGGGAG
52251 ACAGGTTCTA TCCAGAGACT GTTAAAAGGA TTAGTCTTTG ATTACAAGAA
52301 GAACTCTTCT TATACGTGTT TGGGAAGAAA AAATATGTGA GTAGCTATGG
52351 ATAATTTTGC AGGAGGTGGG CAGAATACCA AGATATTCTG CCTGGTGGCC
52401 TCTCTACTCT TCCTTGAGCT CCTGAGAAAG GATGTGATCT GAGAATGAGG
52451 GAGGAAGTGG TATTGGAAGC TGGAGGAGAA TGGAGAAGAT CAAAATGGTT
52501 AGTCTAACAA ATGGGAGAGA ACTGAGATAG ACAAAAAGGAT TTCAGGGTGG
52551 TTTTGAGGGC TCAGTTAAGT CTCCTTTAGG AAGGTTCACT TCTGTAGCCT
52601 TGGCAAGTTA CTTAAAGTCT CTGTGACTAT TACCTCATCT CTAAGATGGG
52651 GACTAAGCTT GGTGACATAG TTTTACATAC CAGGCACAGT GCCTGACTTT
52701 TTGGCTCTGT CCTGAAGTCT TCCCTTTGTA TATGGTATGT TTCGGGGAAT
52751 AGGAGCTCA AGCACTTATC CTTTAAATAT TTATCCTCCA TCAGTCACTA
52801 AACGTTTACT CTGTACTTTT GATAGGTGCT GTGGGGGTCC AGGGTATAAA
52851 AGGTACCTTC AAAGTACTG TTAAGTGCA GGAAGTTTT TAAGCAAATT
52901 ATGTTTAATG ATTTTGACAA TCTGACATGC AGGAAAATTA ATAGGGCCTA
52951 TGCAGAAGAG GAGTTTTATG TAACACTCTG TAGTTCAGGA AACAGAGCCC
53001 TTGGAAGCAG TGATCTCTCT GGGGAGGAAT GTCTGGTATT TGGGAATCTC
53051 ATGAAATGAT AATATACTTA ATTTTATCA TGAGCAGCAA AACACAGATT
53101 TGCTAGGAGA AAGTCATCGT ATGTTGTTGC ATTGGGCACT TTAGATCCCA
53151 GGGAACAGAA ACTGGCTGGC ACAGGAATGG GCATCACTGT GGGGATGGAT
53201 CATGTAGGGG AAGGATCCCT GGAGAAGTCC AGGAGGTGAG ACTTCCCCCT
53251 TCCCTTCTCC ATGCATGAGT CCACTTCTCT CTGTTGACTT TCCCTTGTCT
53301 CCTCTGGTGA CAGCAGCTGC TTACCTCTGG AGACCCCTC ACATTTCTGA
53351 GAGAAGGAAT CTGGCTTGCC TGGCTAATTC CCATGGTCTA TGTTTGGGCA
53401 GAATGCTTFA GCAAGTTGTG TAAAGATAGT GTATTCATAT ATTAATAATA
53451 ATAATAACAT CTAAGTGAACA TTTGCTAGGT GTTCAGACCT GCACTAACCG
53501 TGTTACAAGT ATTATTTTTT TGTAATCCTT TCCATAACCC TGTGAGGTAA
53551 GTAAGTTTAT CACAGACAAG GAAACCACAA TGTGGACCTG TTCATGAAGT
53601 TGCTCGAGGC CACGTGGCTC TGGAGTTCCA GCTCAGGTCT GCCTGACTCT
53651 CAATCCCATT ATATTAATAT ACTGGCCAGT CACTATTTTG GCTGTATTGG
53701 GGTCAATATT ATACCTTGG TCCAGTTAGC TATGTTGGGT CACTTTAGTA
53751 CTGATAGCCA GGGAGATGCT GGGCTTGATA GGTTAGTATA ATTCTATGTA
53801 TTACCTACAA AAAGTGTGTT TATAAATTGT TTTGTTAACA TTTGTTGTCT
53851 ACCTATTTAT TCATTTTATT TGCACTGGTG AAAATAAACT CATCTTTTAA
53901 AAAGTGTGGG GAAAATATCC AAACATTGTG AAAAGTTGAT TAACCTTGTA
53951 TTTTCTGTAC ACCTGGGGAG GGATGCTGTT ATGCTGTTTC AGCAAAGGAG
54001 CAAGTTGGTC CAATCTGGGA GACATCTGTG TTTTGTGGAA ATCTGACTTG
54051 AAAACCACTG TCCAGTCACT GCGTGATTA GCATTTAGGC CTTGCTCTTC
54101 TGCTATGTAT TATTAATGTA GTGTATACAT TTCGAGACAC ATCATCACAT
54151 TTGTCAATTT ATTGATTTCT AGGAGCTGAT TTGTATTCTA GGATTGTCTA
54201 GTTGGCTTGG GCTGCCATAA AATACCACAG TGTGTGTGGA ATCAACAACG
54251 GAAATTTATT TCTAACAGT TCAGAGGCGG GAAAGCCTAA GATCAAGGGC
54301 CAAGCCAGTT TGATTTCTAG TGAGCGTTCT CTTCTCAGCT TGTAGACAGC
54351 TGGTATGTGC TCACATGGTC TTTTCTTGGT GCACATGTGA AGGGGGAGAG
54401 AGAGAGTGGG CTCTCTGGTG TCTGCTCTTA CAAGAACACT GATCCTGTCA
54451 TGAGGGCTCC ATCCTCATGA CCTCATAACC CTAATTACCT CCAGAAGCCT
54501 CATCTCCTAA TACCATCACA TGGGAGGTTA CAGCTTCAAC ATATGAATTT
54551 GGTGGGGGTG CAGCTCAGTC CACAGCAGGT AGTAATGTGC ATTTTAAAC
54601 TTGTTTATAC AGTACAAGAA GTTACTTACT GAAGAAGGAC AAAAAATAGG
54651 AACATTTGAG AGATTTATTT CTGGTTCCAT GGCTGGAGCA ACTGCACAGA
54701 CTTTTATATA TCCAATGGAG GTGAGTACCA TTGTCAAGTC TGACTGTGTG
54751 ATGGTGTTCTG TGTGGTTGT CTATTGCTCT CTAACAAGTT ATCCCAAAT
54801 TAACAGTTTA AAACAAGCAT TTATCATCGC ACAGTTTCTC TGGGTGAGGA
54851 ATCTGGAAGC AGCTTAGCTG GGTGCCTCTG GCTCAGGTT TTTACAGCC
54901 CACAGTCAAG ATGGTAGTCA GAGCTTGGAA TCAGCTGGAG GCGGATTCCA
54951 AGCTCACTCA TGTGCTGCC AGGCCTCACT GGCTATTGGC TGGAAACATC
55001 AGTTCCTTAT CACGTGAGCC TTTCTGTAGG CTGCCTGAGT ATCCTCAAAA
55051 CACAGTAGCT GGCTTCCCTA GAGTCAGTGG TCCAACAGAG AGAGAGAGAG

FIGURE 3-19

55101 AGAGTGCCTA AGATGAAAGC TGGTATCTTT TGCCTCTTCT GCTGTATTCC
55151 ATTGATCACA CAGACCAACC CTGGTAGAGT GTAGGAGGGG CTGGTATAAT
55201 GGTGTTAATA ACCGGAGACA AATATCACTG GGGGTCACCT TAGAGGCTGG
55251 CTGCCACTTT AGAGGCTGGC TGCCATTCTT GTCCAAAGAG TTTCTGTACC
55301 ATAAATTTAA TAATGGAATC TCAGGATTTG ATTATATGGT GATTATCCTA
55351 ATTAGACATC CTTTCATTAG TGCATAGGTT GGCAAAACAC AGACCTACGG
55401 ACTGTTTCAT ACAGCCCTTG ACCTAAGAAT GCCTTTTACA TTTTAAAAAA
55451 GTGGGCAACA CAGGAAAAGT TGAGAAAAGT CTAAAATCGA CACCCTAAGA
55501 TCACAATTAA AAGAACTAGA GAAGCAAGAG CAAACAAATT CAAAAGATAG
55551 CGGAAGACAA GAAGTAGCTA AGGTCAGAGC AGAACTGAAG GAGATAGAGA
55601 CACGAAAAAC CCTTCCAAAA ATCATTGAAT CCAGGAGCTG TTTTATGAA
55651 AAGTTTAACA AAATAGACAA CTAGCCAGAA TAATAAAGAA GAAACCAGAG
55701 GAGAATCAAA TAGCCCAAT AAAAAATGAT AAAGGGGATA TCACCACCAA
55751 TCCCACAGAA ATACAACTA CCATCAGGGA ATACTATAAA CACCTCTATG
55801 CAAATAAACT AGAAAATCTA GAAGAAATGG ATAAATTCCT GGACACATAC
55851 ACGCTCCCAA GACTAAATCA GGAAGAAGCT GAATCCCTGT ATAGACCAAT
55901 AACATGTTCT GAAATTGAGG CAGTAATTAA TAGCCTACCA ACCAAAAAAA
55951 ACCCAGGACC AGACAGATTG ATAGCCGAAT TCTACCAGAG GTACAAAGAG
56001 GAGCTGATGC CATTCTTTCT GAAATTATTC AAACAATAGA AAAAGAGAGA
56051 TTCCTCCCTA ACTCATTTTA TGAGGGCAGC ATCATTCTGA TACTAAAACC
56101 TGGCAGAGAC ACAACCAAAA TAGAAAATTT CAGGCCAATA TCCCTGATGA
56151 ACATCAATGT GAAAATCTC AATAAAATAC TGGCAAACGT AATGCAGCAG
56201 GACATCCAAA AGTTTATCCA CCATGATCAA GTTGGCTTCA TCCCTGGGAT
56251 GCAAGGCTGT TCAACATATG CAAATCAATA TAACGGAATT CATCAATAAA
56301 CAGAACCAAGT GACAAAAACC GCATGATTAT CTCAATAGAT GCAGAAAAGG
56351 CCTTCGATAA AATTCAACAC CACTTCATGT TAAAACTCT CACTAAACTA
56401 GTTATTGATG GAATGTATAA CAAAATAATA AGAGCTGTTT ATGACAAACC
56451 CACAGCCAAT ATCATACTGA ATGGGCAAAA GCTGGAAGCA TTCCCTTTGA
56501 AAACCGGCAC AAGACAAGGA TGTCTCTGT CAGCACTCCT ATTCAACGTA
56551 GTATTGGAAG TTCTGGCCAA GGCAATCAGG CAGGAGAAAG AAATAAAGCG
56601 TATTCAAGATA TTGAAAAGAG AAGTCAAATT GTCTCTGTTT GCAGTTGACA
56651 TGATTGTATA TTTAGAAAAC CTCCTTGTCT CAGCCCCAAA TCTCCTTAAG
56701 CTGATAAGCA ACTTAAAGCA AAGTCTCAGG GTACAAAATC AATGTGCAAA
56751 AATCACTAGC ATTCCTATTA ACCAATAATA CACAAACAGA GAGCCAAATC
56801 ACGAGTGAAC TCCCATCCAC AATTGCTACA AAGAGAATAA AATACCTCGG
56851 AATACAACTT ACAAGGGATG TGAAGGACCT GTTCAAGGAG AACTACAAAC
56901 CACTCCTCAA GGAAATAAGA GAGGACACAA ACAAATGGAA AAACATTTCA
56951 TGCTCATGGA TAGGAAGAAT CAATATCATA TCATAGGAAG AATCAGTGGC
57001 CATACTGCCC AAAGTAATTT ATAGATTCAA TGATATCCCC ATCAAGCTAA
57051 CATTGAATTT CTTACAGAA ATAGAAAAAA CTACCTTAAA TTTCATATGA
57101 AACTAAAAAA GAGCCTGTAT AGCCAAGACA ATCCTAAGCA AAATGAACGA
57151 AGCTGGAGGC ATCAGCTAC CTGACTTCAA ACATACTACA AGGCTACAGT
57201 AACCAAAACA GCATGGTACT GGTACCAAAC AGATATATAG ACCAATGGAA
57251 CAGAACAGAG GCCTCAGAAA TAACACCACA CGTCTACAAC CATCTGATCT
57301 TTGACAAAAA CAAGCAATGG GGAAAGGATT CCTTATTTAA TGTATGGTGT
57351 TGGGAAAACT GGCTAGCCAT ATGCAGAAAA CTGAAACTGG ACCCCTTCCT
57401 TACACCTTAT AAAAAAAAAA TTAAGTCAAG ATAGATTAAA GTCTTAAACA
57451 TAGACTTAAA CTATAAAATC CCTAGAAAAA AACCAGGGCA ATACCATTCA
57501 GGACACAGGC ATGGACAAAG ACTTCATGAC TGAATCACAA AAGCAATGGC
57551 AACAAAAGCC AAAATTGACA AATGGGATCT AATTAAACTA AAGATCTTCT
57601 GCACAGCAAA AGAACTATC ATCAGAGTGA ACCGGCAACC TACAGAATGG
57651 GAGAAAAATT TTGCAATCTA TCCATCTGAC AAAGGGCTAA TATCCAGAAT
57701 CTATAAGGAA CTTAAGCAAA TTTACAAGAA AAAAAACCC ACCAAAAAGT
57751 GGGTGACGGA TTGAACAGA CACTTCTCAT AAGAAGACAT TTATGCAGCC
57801 AACAAACGTG AGAAAAGGCT CATCATCCCT GGTTGTTAGA GAAATGCAAA
57851 TCAAAACCCC AATGGCATAC CATCTCACGC CAGTTAGTTA AAAAGTCAGG
57901 AAACAACAGA TGCTGGCAAA TATGTGGAGA AATAGGAATG CTTTTACACT
57951 GTTGGTGGGA GTGTAATTA GTTCAAGCAT TGTGGAAGAC AGTGTGGCAA

FIGURE 3-20

58001 TTCCTCAAGG ATCTAGAACC AGAAATACCG TTTGACCCAG CAATCCCATT
58051 GCTGGTTATA TACTCAAAGG ATTATAGATT TTTCTACTAT AAAGACACAT
58101 GCACACGTAT ATTTATTGCA GCACTGTTCA CAATAGCAAA GACTTGGAAC
58151 CAACCCAAAT GCCCATCAGT GATAGACTAG ATAAACAAAA TATGGCACAT
58201 ATACACCATG GAATACTATG CAGCCATAAA CAAGGATGAG TTCATGTCCT
58251 TTGTAGGGAC ATGGATGAAG CTGGAAGCCA TCATTCTCAG CAACCTAACA
58301 CAGGAACAGA AAACCAAACA CCACATGTTT CCACTCATAA GTTGGAGTTG
58351 AACAATGAGA ATACATGGAC ACAGGGAGGG GAACATCACA CACTGGGGCC
58401 TTTTTGGGGA TGAGGGGCTA GGGGAGGAAT AGCATTAGAA GAAATACCTA
58451 ATGTAGGTGA CAGGTTGATG GGTGCAGCAA ACCACCATGG CACGTGTATA
58501 CCTATGTAAAC AAACCTGCAC GTTCTGCACA TGTATCCCAG AACTTAAAGT
58551 ACAATTTTTA AAAAGTAGGC AAAAACAAAA GAAAAGAAAA GTAATATACA
58601 ACCGAGACCT AATATTTTAG GCTTGCAACG ACAGATATTT TACTATTTAG
58651 TCTTTACAGG AAAAGTTTTT CAACTACTGC TTTATAGCAA AAATAATATT
58701 GTAGATGTGG AATTTATTGA TATAGCAGAG GGGTTTTTAG TAACTGATGA
58751 CTTAAGCAAG ATAAATACAA TTTTCACCGA TATGTGGTAT GCATGCTAAT
58801 ACAGCTTTTT TTAAGCATCT TAATATGATT GTTTATATTA CTCCACACAC
58851 CTCTCAAAAA ACCTTAATAC CCTATTTTTT CTCTCATATC CTCCCATATC
58901 AGTTAATAGT ATCACCTTCC CAACTCCCCA CTGCCCCATC CTGTGTTCCA
58951 AGCTAGAAGT ATTGGGGTTA TCCTTTATAC TACCATTTCC CTCACCTTCC
59001 AGATGCAGGT GGTCAACAGT CAGTTTTGTT AAGACATCAA TAGATTATCT
59051 TGCTTCCATT TCCTTGGTCA CTTCTTCAT CAGATCCTCC TTGCAGTAAA
59101 CGGGTCTCTC TGGCTTTGGT CTTAGCCCCC CAATAGAGGT AATACATGAA
59151 AGAGAATGTA TCAACAAATT GTACAGTCTT TTGAGTGACA ATATGTGCTA
59201 GGTATTTGTT CCATGTAAAA TTACTTCATT TGAATCCCAT GATGATAGAG
59251 TTAATATGAA CAATCATATT TTGTTTTTTT TTATATCCAG GTTATGAAAA
59301 CCAGGCTGGC TGTAGGCAAA ACTGGGCAGT ACTCTGGAAT ATATGATTGT
59351 GCCAAGAAGA TTTTGAAACA TGAAGGCTTG GGAGCTTTTT ACAAGGCTA
59401 TGTTCCCAAT TTATTAGGTA TCATACCTTA TGCAGGCATA GATCTTGCTG
59451 TGTATGAGGT GAGTTTGTAG AAATCTTTTG AATTGGAAAA TGCAGTTAGA
59501 TCTTGTTAGA ATTGGACTTT ATATGAAGAA GTAGATATAT ACCAGAAAAAC
59551 AGTGTGTGAC CAGAAGTAAA TTCAAGCATG TGTTATTTGA ACTTTCAGT
59601 AACTTGAGTG TGAATATGCA TGGGGTCACT TTTGTATTAG ATTTTCTTGG
59651 GAATTGCTTT TGTTAATGAA GAGTAGACTC AAAGTTAGGT ATAGTTGTTT
59701 ACCTTAAAAG GTGTTTCTAG AGATTTTTTC CTTTGTTTTG GATTTGCAAA
59751 AATCTGACAT TAAGCCAAGT GACTAATGTG ACTAACATGA GTAATACAGT
59801 TTCATTCCCT GTACGGAAGA ATACAAATCT TGGATCAACC CTGCAATCTA
59851 AATCATTTAA TAATTTATGA ATCTCACAAA CAATTATTGA GCACACACTA
59901 TACAAACCAC TAGGTTAGAC ACTGGATCTG GGGATTCAAA GGACTCAATG
59951 TGTGCCTTGA AGAAACTGAA GGTCTGGTGG GGGAGACAAA CGACTAAAAC
60001 TCAGCGTGGT TATCTGTGCT GCGACAGACA TGAGCCAGGG TGCATGTTAG
60051 GATGAGACCT AAGCTACAGC GTAGAGGAAG AGTGGAATGT GTAATGAAAA
60101 GAAGAGTCGA ATTTTTTTTT TAAAGAGCTT TATTGAGATT TAGTTCATAT
60151 TCCTTACATT TCACTCATTT GAAGTGTACA AGCAAATGGT TTTTGGCTTC
60201 TTACATAATT TTTAAAAATT ATTATAAAAT ATAAATTTTG CCATTTTACT
60251 AATTTTAAAG GTACAATTCA GTGGCATTAA TTACATTAC CACATTTGTC
60301 AACCATCAAC ACTATTTCCA AATCCTTTTC CTCACTCAA ACAGAAACAC
60351 CTTAACCTTT AAGCAATAAC TTCCTACCCT CCGTAACTCA AACCTTTGGT
60401 AACCTCTAAT CTGCTTTCTA TGTCTAGGAA TTTACCCATT CAAGATATCT
60451 TATAAGTAGA ATCATACAGT ATTTTCTTT TTGTGTCTGA TTTATTACTC
60501 TTAGCATAAT GTCTCTAAGG TTTGTTTCATG TTGTAGCATG TATCAGAACT
60551 TCATTTCTTT TCATGGCTGA GTAATATTCC GTTATGTGTA TATACCACAT
60601 TTTGTTTAGT CCTTCATCTG TTGAAGAGCA TTTGGATTAT TTCTACTTTT
60651 CCAACATTGT GAATAATGCT GCAGTGAACA TTGGCATCTG CGTATCTGTT
60701 CGAGTCTATG CCTTCAATTC CTTTGGGTAT ATATCTCAGA ATGGAATTGC
60751 TGAGCCATAT GGTCAATCTG TGTTTAGCTT TTAGGAACTA TGAGACTGTT
60801 TTCCATAGTG GCTGCACTTA CATTCTCACC AGCAACATAC AAAGGTTCCA
60851 GTTTTTCCAC GTCCTTATTA ACACTTAATT TCCATTTTAA AAAAGCTTAT

FIGURE 3-21

60901 TTTTATTATG GCCGTCCTCT TAGGTGTGAG GTGGTATGGT TCAGGACTTT
60951 ACTTCTTG TG CTGAGTTTTT TAAAAAATTG TGATTAACAA CACATAACAT
61001 AAAGTTTATG ATTTTAAACCA TTTTAAATA TATAGTACAG TAAGTGTTAA
61051 CTGTTTGTGG TTTGTTGTGC AACAGATCTC TAGAACTTTT TCACTTCTCA
61101 AAACCTAAAC TCTATAGTCA TTAACAACA GCTCCCAATT TCCCCTTCAC
61151 CCCAGCGCTG TGTAACTAC TTTCTCGTTT TATGAGTTTG ACTACATTAA
61201 ATACCTTGTA TAAGTGAAAT CATGTGGTAT TTCTCTTTCC GTGACTGGCT
61251 TATTTTCATG AACATAGTTT CCTCATGATT CATCCATATG ATAGCATACA
61301 ACAGGACTTT TTTGTTTTTA AGGCTGAATA ATAATTTGTT GGGTATATAT
61351 ATCACAATTT CTTTATTCAT CTGTTGATGG ACATTTGGAT TGTTTCTACA
61401 TCTTGACTAT TGTGAATAGT GCTGCAGTGA ACATGGTTGT GCAAATATCT
61451 CTTCAAGATA CTGTTTTTCTG TTTCTTTTGA CATATACTCA GAAGTGGAAT
61501 TTCTGGGTCA AATGGTAATT CTATTTTTAA GTTTTTTGAGG AACCTCCATG
61551 TCATTTTCCA TAGTAACTAG ACCTTTTTGT TTTTAAACAT TTCTATCAAT
61601 GTACACCAAG ATTCCAATTT CTCCATGTCC TCCCAACAC CATTAAGTGG
61651 GGTGGTGGTC TACTACTATT GCTGTGTTGC TGTTTATTC TCCCTTCAGT
61701 TCTGTAAGTG TTTGCTTCAT ATATTTAGGA GCTTAATATT AGGTCCATAT
61751 GAAGTTATAA TTTCTTCTG GATAAGTGAC CCATTTATCA TTATGTAATG
61801 TCCATCTTTG TCTCTGTGA CAGTTTGTGT CTTAAATCT ATTTTGTCTG
61851 ATGTAATTAT GGCCACCCCT TTTCTCTTTG GGTTCCTGTT TTTATGGAAT
61901 ATCTTTTCC ATCTTTTCC TTTTCTCTTA TGTGTGCTCT TAGATCTAAA
61951 GTGAGTCTCA TAGATAAGGT ATAGTTGATT CTGTATGTGT TATTCATCA
62001 GCAATTTATA TCTTTTAGTT AGGGGATTTA ATCCATTTAC ATTTAAAGCA
62051 GTTACTGATA GGGGAAGGACT TACTGTTGTC ATTTGGCTAG CTACCTTTTT
62101 ATCTTTGTCC TGTGGCTTTT CTGTTTTTCC CTTCCTCTCT TCCTGGCTTC
62151 TTCTGTGTTT TGTGATTTT TTTTTTTTT GTAGTGATAT GTTCTGATTC
62201 CCTTCTCATT TCCCTTTGTG TGCACTCTAT AGATGCTATT TTTGTGGTTA
62251 CCATTGCAAC TACATAAAGC ATACTAAAGT TATAGCAACT TATTTAAGC
62301 TGTTTACAAC TTAACCTCAG TGGTATATAA AACTCTATTT CTTTACATAT
62351 TTCACCTCCT CCCCACAAAC TTTATGTCTT TTGATATTGT ATATCCTTAA
62401 CATAGATTTA TTATGCTTTT TTTCTTTAAA TTCTGTTTAA
62451 ATTTTGTITT TGAAATTTAG ATTTTCAAGT TATTTATATA CCTTCATTAC
62501 AATACTATAG GATTTTATAA TATTCTAAAT ATTGACCTTT ACCATAGAGT
62551 TTCATATTTT GTGGTTTTGT GTTGCTATTT ATCATCCTTT TGTTTCTCCT
62601 TTTAGCCTTT CTTGTAGGGC CGGTCTAGTG GTGATAAGCT GTATCAGCTT
62651 TTGTTTGTCA GGGACAGTCT TAATTTCTCC TTTTTTGAAG GGCAGTTTTG
62701 CCCATACAGT ATTTTGTITT GGCAGTTTTT TTAAGTTTCA AAACATAGAA
62751 TATAACATTC CATTTCTTTC TAACCTGCAA GATTTCCATT GAGAAATGCA
62801 CTCAATGGAT TTTTAAATCC ATTGAGATAA TTTTAAATC CTGTAGGATT
62851 TAAAAATTTT AGTCTTACAG GATTAACAAA TTAAGGTT AAACCTGTGA
62901 TATAACATAT TAACATGTAT TTTATACTTA AAGTATCTTA TGTTTAAAAA
62951 GTTGATTATC ATATATATTT TATACAGTTT CTCCTAATTA TTGCCTTCTA
63001 ATGAAATACA GGGACCTAGA GTAACAGGGA TAAAGTATGG CCTTTTGATC
63051 AGCACGCCTG GTTCTGAGTC CTTCTTAAAA AACTCTGGG CCTGGTGTGG
63101 TGGCTCATGC CTATAATCTC AGCACTTTGG GAGGCCGAGG CGGGCGGATC
63151 ACCTGAGGTC AGGAGTTTGA GATCAGCCTT GCCAGCATGG TGAAACCCTG
63201 TCTCTACTAA CAGTACAAAG ATTAGCTGGG CGTGGTGGTG GGTGCCTGTA
63251 ATCCAAGCTA CTCAGGAGGC TGAGGCAGAA GAATCGTTTG AACCTGGGAG
63301 GCAGAGATTG GGCCACTGCA CTACAGCCTG GGTGACAAGA GCGAGACTCC
63351 ATCTCAAAAA AACAAACAAA AACTCCGCTG AGATGAATTT TTCTCATTTT
63401 TAAATCAGA ATAATAGATT TATGTAAGAG TTTCTGTAAG GCTCAAATGA
63451 AATATATGTA ACGTGTAATA TGAGATACAA TTAGTAGAAT TATATTATTT
63501 TATTAATACT CACCATAAGA GGTGTTCTTT AGATCCTGCA GCGTTTGCTG
63551 CGCAGTTTCA GTTTGTTTAG AAGAATGTCA GTAACCGGTG CAAACCTCAT
63601 GTGTTCCGCA CCCCCAGTGG CCTCCACCT CTCCACAGAG TCACCGCCTC
63651 CTGCAGTGCC TGCTGCTTCT GCAAATGCGT GGCCTCATCC TGCAGAAACG
63701 GGGCTTCTCA TGAGGTTGAG AATAGCTGTG AAAATGTTTA CGTTGAAGTT
63751 GTAGAGTTCC TTAATTATTT TCTTCTTTAT TTCTCTGGCA GCTCTGAAG

FIGURE 3-22



63801 TCCTATTGGC TGGATAATTT TGCAAAAGAT TCTGTAAACC CTGGAGTCAT
63851 GGTGTGCTG GGATGCGGTG CCTTATCCAG CACCTGTGGT CAGCTGGCCA
63901 GCTACCCATT GGCTTTGGTG AGAACTCGCA TGCAGGCTCA AGGTGAATTT
63951 TTGATTACAG AACCACACCG ATAAAAGTGC TGCACCACTA ATGTGCTTTT
64001 AGAACTCCAA GTTCTACTAA GATGCAGACT GTAGTTTTAA GACAGTATTT
64051 CTCAACCTTT TTTTCATTAT TGCCTCCTTA AGGAATCTTT TCAGAAATTC
64101 TTTTTCTAAA TGCTCCCTCG TCATGAAATT TTAATGCGAC AGAAGCATTG
64151 CATATGTACT GTATGCATAC ATATGCCTTA TAGATAAACA GAGTACTATT
64201 TTTTTTGACT GTGTTACATG CACGTTTTAA GATTATAAGC TTTAGTATCT
64251 GATGGATTTG GGTTCCAGATC CTTGCCTCAG ACTTCTTGGG GTTTTTAATG
64301 GGAATGAAAA TTGTACAGTG TTGTAAGAAT TACCAACAAT ATAAATAAAG
64351 CATCTTGGGT TTGTTAAATT TTTGGTAAAT GGTGGTTGGA ATCATTTTTT
64401 AGTGTTCGT AGACCCTACA AGTTTTGAGC TGTGATTCCT CCTCACTGTG
64451 AACTGTCTC CATTGTTGGC TTTGATTACA CTGTACCATC CTGGTTGTTC
64501 TGCCAGCCCA TTGATAACTT TTACCATTG CTGGCTTTTA TTGCTATCCC
64551 CACTCTATTA AAGTATGCAT TCAAATGCCT TTCTTTTCTC TTTGATGCTT
64601 TCCCTGGTCA GTCTTATCCA TTGTTTTCTT AAGTAGTACA CCTTGGGCAT
64651 CTACAGCTCT ATTCCTCAAC TCCCTTCCAA GTGCCAGCCA CAGCAACCCC
64701 AGCCAAGCAG TCAGTAACTA ATTGGCAAAT ACTCCCTGAG CCATTGTCCC
64751 ATTCTAGACA CTGCCAGATG CTAGGGGTAG AGCAGTCAAC AAGTCAGGTG
64801 TGGCCCCGCC AGTGTAGAGT AGAGAAGACG TTATGTCCAG CAAGTAAACA
64851 ACCTGGTTAA ACCAACTCCT CTTTTGTTAG GGGAGCACAG AGCAAGGAGC
64901 TATAACCTAA CTTGGGCGCT GCAGAATGCT GTCAGTGAAG CTGAGACTGG
64951 AAAGATGAGT GGGAGTTAGC TGGGCACAGG CCAGTGGAGT GGGAAACAGAA
65001 AACATTCCAG TTGAGGGAAA GCATGTGTGA AGACACTGAG GCAGGCACCA
65051 ACATGGTGTA TTTAAGGAGC TGAGAGACAG TCATGGCTGT AGAGAAAAAC
65101 ACAAAGTAGT GAACTACACG TTTCTTGTGT ATTCTCTCAT TTCACCATCA
65151 TAACCATCTT GGGGATGGGA ATACTAACAT TATCCCCATT TTTCAGATGA
65201 GCAACTGGGG CAGAGAGAAT TTAAGTAACT CCCACAAGAT TATACCTGTG
65251 GTAAATGGG GCTCTGATCC GCACTGAAAT TCAGACACAT GCAGTCTGAT TCTAACCCCTC
65301 CTGTCTGCCA GGTCTGATCC AGAACTTTGC ATGACTGATA CGGCTGATAG
65351 ATTGTCTATG GCTGATAGAC TGTCAATTTCT GACCTAAAAG TCTGATCATT
65401 TTACATCTGT TCAGACATCT TTGCAGCCTT TCGGTGTCAG TTCCAAAGTT
65451 GTTAGTGGGA ATTTCAAAGC CTTTAATAAT CTAGCCCCAC TTTGTTCACT
65501 CTCTGTGTAA TAACCACATA CAACAATTGG CTGCATCTCC ATAGCACATG
65551 GTA CTCTCTCC CGTTGTCTTG GTTGTGCCAG CAACACTGGT TTTGCTTTTC
65601 TCTTCTGCT TGTGAGGTC ATTTCCAAGG CCCAGGTCTT TGTGCTTTTT
65651 CCAAGCTTC CCAGAGCTTC TTCCATACTC CCCTTACTTC CTGAGATTTA
65701 ACTGTTCTCT CTTCAGCGCT TGTCTAGTAA GAAGGAGGCA GCAGCAGCAC
65751 TGTGGGGTGG TGGAAAGTGT ACCAGCTTTG GAGTCAGACC ATTGGATCTC
65801 AGCCCTACCA TTTTCTACTT AGATTTTTTT AGGACAAATT TCTCCATCTT
65851 TCTAAGCCTC CAATTGCTCA CTTACAAAAT TGATATAACA TTTACCTTGC
65901 AAGATTGGTA TGGAAGGTAA TTAACCCAGT ATTTAGAACA TAGTAATTAA
65951 TAAATAACTA TTATTACCAT CATTACTATA GTTAGGACAC TCACTGTTAG
66001 GTGCTATACA AAGAGGATCA TAAAAGGGAT GTTGTCTTGG GCTTCTTGGA
66051 ATAAATGTTG TCCTTTTACT GTATTTTAGA ATATCATTCT GGGTCATAAT
66101 TGTTTGTGT CATAATAATG AAACATACTT GAATATTAAA TTACCCTCTT
66151 TTTTTATTTT TTAGCCATGT TAGAAGGTTT CCCACAGCTG AATATGGTTG
66201 GCCTCTTTTG ACGAATTATT TCCAAAGAAG GAATACCAGG ACTTTACAGA
66251 GGCATCACCC CAAACTTCAT GAAGGTGCTC CCTGCTGTAG GCATCAGTTA
66301 TGTGGTTTAT GAAAATATGA AGCAAACCTT AGGAGTAACC CAGAAATGAT
66351 GTTGCAATTT TTGCTTTAGC CTGATAATTG AAACCTTCAA CAATCTCTGG
66401 AGTGACTTTT TCTCCTCGAA TTGAAACAAG TCTATGGCAA AAGAAGCTGC
66451 ATTTTCTTCA CAAAAGGGAA GATGGTAACA ATGGTCACTT CAAACTTTTG
66501 GGCTAAATTA TATGTACACA GAAATGTTCA AAATCATAGT TTTAATGTGT
66551 TTTGAAAAGG CCACACAATT ATACTTTATC TTTTCTTAAT AATCCTGCAA
66601 ATCTCTGCCC TGAATCCGAA ATCTGAAAAT GTACTGGCTT GAACAAAATT
66651 TGTTTTGTGT GTTAGAGTTA TAAATCATTA ATCTTTATTT CGGGTGGTTT

FIGURE 3-23



66701 ACGTTTATGC CAGTTCCTTT ATATTTAAAT TTCTTGTTTT ATATATTTTG
 66751 AATGTCCTTA TAGATTTCTT TAAATTTCTT TATAGAACCA TTAATAGAAA
 66801 ATCATTACAT TTTAAATATA CCTTACAGCA AAAGCATCCA AATAAGTATA
 66851 GGGTTTATGT CCTTATTTTT CTTTCAGCTG AATACGAATG AGCACAGTGG
 66901 TGGAATTTCT GAAGGGAAGT GATGAAATTA TATTTATTTT AGTGGGCACT
 66951 TTTCCATTTT ACCACTGTAC CATTATTTGG TTCCTGGAGT TATACACTAA
 67001 TTTTCAGTAT ATTACTGTTA AATTACCAAC ACAAGGCAAT TTATTTGAAA
 67051 GATTCCGTTT ATCCTGCCAT TGCTTTGAAA AGCAGCAGGA AACGAAATCC
 67101 TTTGACTTGT ATCAGCTTCT GCAGAGCATC TTTGTTTTCC TTTGTCCTTT
 67151 GTTTCCTACC TTTTGAATCA GATTCCGTTT TAGTCAGGAA GACTTCTTGG
 67201 GACCATTCTT AGTAACCTGA AATTTCTTTT TTAATTGCAT GAAGTGGATT
 67251 GATCATGAGC AAATGATGTG CTTATTTCTC CCTCACTGTT GAATATCTTT
 67301 GAACTTGCTG TTTTCAATAT GGGCAGCACA AAGGTGAGAG ATACATATTA
 67351 ATAGTAGTAT GTATTACTCT TATACATTAG ATACCTATAT TTAAATGAAA
 67401 GGCCCAATTT GTAAACATAT ACATTCATAT TCTCTCTTGC CCCAAGTTTT
 67451 AGGAACATGT TAGGATATAG GAGACTTAAT TTATAATAAT GAGAGCATTT
 67501 TTTTATTTTA CTAAAGCCAT TTTTATAGTC AACTATCTTT TCTTATTTGT
 67551 GTGATTAGAA CTTAGAAAAA TATTTACTAG TTGAAGTTAT TATCAGTTTT
 67601 TAATTTAGTT CTTAAACTCA TTTCACTTCT AATAATTTCT GTTATAAATT
 67651 GCCAGCATTT TAATGAAAAT CTAATGATGT AATAGGCATT TTCTTTATTT
 67701 GAACCTACCT CTTTTATTTT CTGAACCAA GAGAAAGATG GACTGGTGTT
 67751 TGTGAAACAT TTTTAAAAAT GTAGTTTCAT TTATATTAGT TATGTTTGAT
 67801 AAATGTCTCA GTATTTTAT AATATGATAA GCCTGGGATT CTACTTTTAG
 67851 GGTATTTTGT ACTTTTGAGT AATATATAAA GTGACAATAT TAAGGTACAT
 67901 GATCAGCTCT TTCTATTTT ACTCGTAAAA ATTATGGAAA TGAATAATTT
 67951 TGCTAACAA CTTTGAAATT CAACTTCTG GAAAATATGA AAATATTCAT
 68001 TGTTCAATTAT GAATTTAAAT TGTAAGGTAT GAATGTGATT TGTCTGTACA
 68051 TCTTGTATCT TTTCCAAAAA ATGATTCTGT ATCTTTTGGA AAAAAGCCGA
 68101 GAGTTGAAGA TAGTATATTT CTGGTAGTAC TGAATATTTA CTTACAGTTT
 68151 CTATCAAAAA TATATATTTG TTTCTAAAAA TACTTGTTTT CCAGTTTTTA
 68201 TTTTTTTTAG AGAAAAATTCT TAAGTCTCAG TTTCTAATT GAAAAAATAA
 68251 AATTATAAAT AAAGCAAAAA TTGTATCCTA CAGCTTAGCT AGCTTAGATG
 68301 TTTGGCACCA GTTTGAATCA TGCTTTTTTAC AGCTGGCTCC ATGTAGTCTT
 68351 TCCAAACATT TTGGCCTTTC CTGAGCAGCC CTTGTAGATA TTGTCTGTAT
 68401 GATGCATTTT GACACAAGGT GATATTTTTT GTGATATCAA AATTCCACAT
 68451 TTACCCATTA GAGTTACAGC CCTGGGGTTC ACAGTACCAA GGGGGACCCA
 68501 GAGCCTCAGG ATTGGCCAGG CTCATTTTGC CGTGGAGTAT CAGTTTGTCT
 68551 TGAAATTGTG GGAAAAAATT CTAAGTTGAA TTCCTGGTA AGTAATTTTT
 68601 TAAAATTTCA TAATGCAGAT TACATCCAAA ATTTGATTTA AAAATTAATA
 68651 CATAAGACTG CAGAGAAATT CTGCATTTCA ACTCCAATAC TATCCAGACT
 68701 TCAGAAATAA CTTATCAGTT ATTTCTGTAA GCTTCTTGCT TACCTGGATA
 68751 CCTGACAGGT GAGATGGCTG TAGCAGACAC TGGCAGTCC CTGCCCACAC
 68801 ACCTGTCCCT GTCCACAGCT GCACAAGGCA GCTCTGTGTG CAATTGCCAG
 68851 CATCTGCTCC TCTGTTCTCA GGAATCTTT GTTAGAAAA TGCTGCCATA
 68901 TTTGTTTCTC ACCTATTAGT CTTGTCTCCC AGTCAAGAGA ATAAATTTAT
 68951 GCAAGCAGAG ATTGTACTTT ACAGTATTTT GTCTTTGAGC TTGGCATTAG
 69001 GTTGCAATTTG TAAAAATGTG GCATGGCTTC CTCATCCCCC AATAGGAAC
 69051 TTGCCAGCCC TTTTGTCTC ATGGAACCTC CTTTTTTGAA AAGAGCACCA
 69101 AAGGAGTAAA AATACTGTGG AGGGAGCAAC CCTCCTTTGC CATATGCTCT
 69151 CATTGGGAGA CATGTGGAGC AGTCTGAAGT CATTTAGGCC ACTCTCTGGG
 69201 AGAGCACATC CTATGATGTT CTCCAGCCT AGCCCCTTCC ACTGTGCTCA
 69251 AGTCCAAGCT GACCAGCTTT CTGACCACAG TGTAACAAA GATGATTGTC
 69301 AGTGGGCCCC AGAATCCTAT ACCCAGA (SEQ ID NO:3)

FEATURES:
 Start: 2132
 Exon: 2132-2314
 Intron: 2315-17055

FIGURE 3-24



Exon: 17056-17182
Intron: 17183-20983
Exon: 20984-21071
Intron: 21072-41719
Exon: 41720-41831
Intron: 41832-45391
Exon: 45392-45550
Intron: 45551-47878
Exon: 47879-48031
Intron: 48032-54612
Exon: 54613-54720
Intron: 54721-59290
Exon: 59291-59458
Intron: 59459-63791
Exon: 63792-63942
Intron: 63943-66164
Exon: 66165-66346
Stop: 66347

CHROMOSOME MAP POSITION:
Chromosome 1

ALLELIC VARIANTS (SNPs):

Position	Major	Minor	Domain
1722	G	C A	Beyond ORF(5')
1767	C	G A	Beyond ORF(5')
1840	C	G	Beyond ORF(5')
1857	T	G	Beyond ORF(5')
1945	G	T	Beyond ORF(5')
2007	A	C	Beyond ORF(5')
2769	C	G	Intron
3664	C	T	Intron
3827	G	A	Intron
4113	C	T	Intron
4337	A	G	Intron
4473	G	A	Intron
6455	T	G	Intron
6533	T	G A	Intron
6919	G	C	Intron
7305	G	A	Intron
7340	A	G	Intron
7466	A	G	Intron
7589	G	C	Intron
7810	A	C	Intron
9104	G	A	Intron
9503	A	T	Intron
9898	G	C	Intron
10196	T	C	Intron
12327	C	G A	Intron
13749	G	A	Intron
14150	T	C	Intron
14529	G	A	Intron
14653	G	A	Intron
15871	A	G	Intron
19244	G	A	Intron
19387	T	G	Intron

FIGURE 3-25

19447	C	G	Intron
20076	T	C	Intron
20492	T	-	Intron
20868	T	C	Intron
20941	T	C	Intron
21116	C	T	Intron
21701	G	A	Intron
21710	A	-	Intron
21826	C	T	Intron
21840	-	T	Intron
21841	-	C T	Intron
21843	-	C	Intron
22045	C	A T	Intron
22061	G	T	Intron
22348	-	A G	Intron
22682	A	G T	Intron
22783	-	T	Intron
23448	A	G	Intron
24960	G	A	Intron
24983	T	C	Intron
25390	T	C	Intron
26060	C	T	Intron
30245	C	G	Intron
33664	G	T	Intron
33883	C	A	Intron
34373	G	A	Intron
34558	G	T	Intron
43929	T	A	Intron
44309	T	- C	Intron
44997	T	G	Intron
46538	A	G	Intron
48153	T	C	Intron
48288	G	T	Intron
48412	G	A	Intron
48446	C	G	Intron
48456	G	C	Intron
48789	C	-	Intron
48859	G	C	Intron
49126	A	G	Intron
49378	T	G	Intron
49482	A	C	Intron
49741	G	A	Intron
49840	A	G	Intron
50102	G	A	Intron
50109	C	G T	Intron
50747	G	A	Intron
51272	G	A	Intron
52842	G	A	Intron
61837	A	G	Intron
62018	A	G	Intron
65562	A	G	Intron
65780	G	A	Intron
66092	G	A	Intron
66617	C	T	Beyond ORF(3')
66892	G	A	Beyond ORF(3')
67263	G	A	Beyond ORF(3')
67651	G	T	Beyond ORF(3')
67935	C	T	Beyond ORF(3')

FIGURE 3-26



69000	T	G	Beyond ORF(3')
69134	C	T	Beyond ORF(3')

Context:

DNA
Position
1722

TTGCCCACGCAGATGGCTGTTGATCTTTCTGCAACAAATCCAGGAGTTTCTCCTTTTTG
TTTTATAATTGCTCCAATAGATGCTTTAGGATTTAACTCTCTGCTTTTTAAAGCAGAATC
GCCATCCCAGGTGTGCAACCACGAAAAAATTAGACATCCGTGAGAGACAATGCCCTCCAT
GGCCAGTTTCCAGGCAGAGAGAAGCAGCTCTGGGCTGACCGCCAAGGCTCCGGCCCGAG
AGGGTCTTTAAGTGGAGTAACCACTCTTCAAGACCCCGCTCCAAGCCACCGACGCGCTG
[G,C,A]
CGCTGCAGCCCTGGACCTGCTGGGGGCCTCTTCTCGGACCCGCATGCTGACAGCGGGAC
TGGCAACTGGGCAGAGGTGACCCCGGTCCGCACAGCACCTCCCGAGACCCAGCTCCCA
GCTCCCTCACTTCCGGCTCTCTGGAGGCGGGCCCGCCAGTGCCGCGGAGGCCAGCGCGG
CGAGTCTCTCCCGAGCAGCGGCGGGACGGCCACACCTGCGCGCCGCGCGGGCTCGGGTG
GGGTCTCCGCTCTGCGCCCTGCGCGCCGACCGCCACCCCGACGGCGCCCCAAACGCT

(SEQ ID NO:35)

1767

AGTTTCTCCTTTTTGTTTTATAATTGCTCCAATAGATGCTTTAGGATTTAACTCTCTGCT
TTTTAAAGCAGAATCGCCATCCCAGGTGTGCAACCACGAAAAAATTAGACATCCGTGAGA
GACAATGCCCTCCATGGCCAGTTTCCAGGCAGAGAGAAGCAGCTCTGGGCTGACCGCCA
AGGCTCCGGCCCGAGAGGGTCTTTAAGTGGAGTAACCACTCTTCAAGACCCCGCTCCAA
GCCACCGACGCGCTGACGCTGCAGCCCTGGACCTGCTGGGGGCCTCTTCTCGGACCCGC
[C,G,A]
TGCTGACAGCGGGACTGGCAACTGGGCAGAGGTGACCCCGGTCCGCACAGCACCTCCC
GAGACCCAGCTCCCAGCTCCCTCACTTCCGGCTCTCTGGAGGCGGGCCCGCCAGTGCCG
CCGAGGCCAGCGCGGCGAGTCTCTCCCGAGCAGCGGCGGGACGGCCACACCTGCGCGCC
GCGCGGGCTCGGGTGGGGTCTCCGCTCTGCGCCCTGCGCGCCGACCGCCACCCCGAC
GGCGCCCCAAACGCTGTTGCGCCGCGCGCCCGCCAGCCCGGCTCGCGCTGGTCCCGG

(SEQ ID NO:36)

1840

TCGCCATCCCAGGTGTGCAACCACGAAAAAATTAGACATCCGTGAGAGACAATGCCCTCC
ATGGCCAGTTTCCAGGCAGAGAGAAGCAGCTCTGGGCTGACCGCCAAGGCTCCGGCCCG
AGAGGGTCTTTAAGTGGAGTAACCACTCTTCAAGACCCCGCTCCAAGCCACCGACGCGC
TGACGCTGCAGCCCTGGACCTGCTGGGGGCCTCTTCTCGGACCCGCATGCTGACAGCGG
GACTGGCAACTGGGCAGAGGTGACCCCGGTCCGCACAGCACCTCCCGAGACCCAGCTC
[C,G]
CAGTCCCTCACTTCCGGCTCTCTGGAGGCGGGCCCGCCAGTGCCGCGGAGGCCAGCGC
GGCGAGTCTCTCCCGAGCAGCGGCGGGACGGCCACACCTGCGCGCCGCGCGGGCTCGGG
TGGGTCTCCGCTCTGCGCCCTGCGCGCCGACCGCCACCCCGACGGCGCCCCAAACG
CTGTTGCGCGCGCGCCCCGCCCAGCCCGGCTCGCGTGGTCCCGGTCTCGCCCCGAG
CCCTCGATCTCCCGTGACTTCTCGGCCAGGCGGCTGCGCTCTGGGACCATGTTGCGC

(SEQ ID NO:37)

1857

CAACCACGAAAAAATTAGACATCCGTGAGAGACAATGCCCTCCATGGCCAGTTTCCAGG
CAGAGAGAAGCAGCTCTGGGCTGACCGCCAAGGCTCCGGCCCGAGAGGGTCTTTAAGTGG
AGTAACCACTCTTCAAGACCCCGCTCCAAGCCACCGACGCGCTGACGCTGCAGCCCTGG
ACCTGCTGGGGGCCTCTTCTCGGACCCGCATGCTGACAGCGGGACTGGCAACTGGGCAG
AGGTGACCCCGGGTCCGCACAGCACCTCCCGAGACCCAGTCCAGCTCCCTCACTTCC
[T,G]
GCTCTCTGGAGGCGGGCCCGGCCAGTGCCGCGGAGGCCAGCGCGGCGAGTCTCTCCCGAG
CAGCGGCGGGACGGCCACACCTGCGCGCCGCGCGGGTCTGGGTGGGGTCTCCGCTCTG
CGCCCTGCGCGCCGACCGCCACCCCGACGGCGCCCCAAACGCTGTTGCGCCGCGCGCC
CCGCCAGCCCGGCTCGCGTGGTCCCGGTCTCGCCCCGAGCCCTCGATCTCCCGTGA
CTTCTCGGCCAGGCGGCTGCGCTCTGGGACCATGTTGCGCTGGCTGCGGGACTTCGT

(SEQ ID NO:38)

1945

CAAGGCTCCGGCCCGAGAGGGTCTTTAAGTGGAGTAACCACTCTTCAAGACCCCGTCCC
AAGCCACCGACGCGCTGACGCTGCAGCCCTGGACCTGCTGGGGGCCTCTTCTCGGACCC

FIGURE 3-27



- GCATGCTGACAGCGGGACTGGCAACTGGGCAGAGGTCGACCCCGGGTCCGCACAGCACCT
CCCAGAGCCAGCTCCAGCTCCCTCACTTCGGCTCTCTGGAGGCGGGCCCGCCAGTG
CCGCCGAGGCCAGCGCGGCGAGCTCCTCCCCAGCAGCGCGGGACGGCCACACCTGCGC
[G,T]
CCGCGCGGGCTCGGGTGGGGTCTCCGCTCCTGCGCCCTGCGCGCCGAGCCGACCCCCG
ACGGCGCCCCAAACGCTGTTGCGCCGCGCGCCCCGCCAGCCCGGCTCGCGCTGGTCCC
GGTCTCGCCCCGAGCCCTCGATCTCCCGTGACTTCCTCGGCCAGGCCGCTGCGCTCT
GGGACCATGTTGCGCTGGCTGCGGGACTTCGTGCTGCCACCGCGGCTGCCAGGACGCG
GAGCAGCCGACGCGCTACGAGACCCTCTTCAGGCACTGGACCGCAATGGGGACGGAGTG (SEQ ID NO:39)
- 2007 GCCACCGACGCGCTGACGCTGCAGCCCTGGACCTGCTGGGGCCTCTTCCTCGACCCGC
ATGCTGACAGCGGGACTGGCAACTGGGCAGAGGTCGACCCCGGGTCCGCACAGCACCTCC
CGAGACCCAGCTCCAGCTCCCTCACTTCGGCTCTCTGGAGGCGGGCCCGCCAGTGCC
GCCGAGGCCAGCGCGGCGAGCTCCTCCCCAGCAGCGCGGGACGGCCACACCTGCGCGC
CGCGCGGGCTCGGGTGGGGTCTCCGCTCCTGCGCCCTGCGCGCCGAGCCGACCCCCGA
[A,C]
GGCGCCCCAAACGCTGTTGCGCCGCGCGCCCCGCCAGCCCGGCTCGCGCTGGTCCCG
TCTCGCCCCGAGCCCTCGATCTCCCGTGACTTCCTCGGCCAGGCCGCTGCGCTCTGG
GACCATGTTGCGCTGGCTGCGGGACTTCGTGCTGCCACCGCGGCTGCCAGGACGCGGA
GCAGCCGACGCGCTACGAGACCCTCTTCAGGCACTGGACCGCAATGGGGACGGAGTGGT
GGACATCGGCGAGCTGCAGGAGGGCTCAGGAACCTGGGCATCCCTCTGGGCCAGGACGC (SEQ ID NO:40)
- 2769 TGGGGCCGCGACCGGCGACCCCGTAACAGAAGTGGGTGATAATACGAAAGTCTACTGGT
ATTTGTCCAGATAAAATGAGTGTTGTGGACACTTGCGCCACGGGCACTGTTAAATTTT
AAGACACTTTTGTCTGAATCCATCCCAGGTTCTTTGTTTTCTGTTTTAATACCTTGCA
ACATGTAATCCGTTTTAGCTGTCAGACTTCAGTGGGTCCCAAGTTTTGTATAAAGCGCA
CACATTGATCTCTTTGAAAGCTGCTTTGTTACAGCAGCTATGTGTATTGTCTACTGTTT
[C,G]
AAAACCTGTTTGAAACCAATCGCGTGTTCCTGTTGAGAAGGAATGGCGGC
ATTCATTGTTTAAGACATTCTAGGTTAATGCCCTAGGTACATAAATTGATCTGAAGGG
TTGACTTGACCTGCGACTGAGCAATTTCAATTTCTCTGAGTCATCTTAAGTGTGCCCTG
AACTTCTGCCCCCTTAGTAGGGTGGAGATATGTGAACTTCTCCAACCCTGTGAAGCGT
TCCCTGACACTGGCATTCTCTTATCAAAGAGGGAAAGTGATTAGGTTACTATGAGGGCC (SEQ ID NO:41)
- 3664 GCTGATTGTCCAGAAATGGCCAGTTGGAGTTCCCCACCATGTCCAATCATTGGCTGGA
AGCAGCCAGGAAAGGGACGACCTTGCTGCAGTGCATCAGCAGATGCCAGGGTTAGAGGC
TAGAGAGTGGAAGTCAACTGTGTTCTCACAGTAGGTGCCCTTTGAAGGGAGATCTCAGTG
GTACAACTCCATGGTCCCTACAATATACAAAAGCTCTTTGGAGTGCTCAATGATTTTTAA
GATTGTAAAGGGATCCTGAGATCAAAAAGCTTGAGAAATTGCTGCTGTATCACCATTTTTA
[C,T]
GTAAGTGCATCATATTCTGTTATATGTTTGTGTCATAGTATATGTTACCAATTCTTTTTA
AATCACCTTTTACTTTATTGATAGTTTAAAAACGATTGTAAGTGAAATTGCAATGGATGT
CCTTTGTATTCAATTTCTCATTCTGGTCCAGTTACTTTGAGGATAAATTTGAGGAGT
GGACATTGCTGAGTCTGAAGGTAACACACATTTTAACTGGGATACGTATTGCCTTTGCG
AAACCTTAGACCCATTTTCACTCTTTGACTGACAGTGCTTGCTTCTCCATCCTCGCT (SEQ ID NO:42)
- 3827 GAAGGGAGATCTCAGTGGTACAACCTCCATGGTCCCTACAATATACAAAAGCTCTTTGGAG
TGCTCAATGATTTTTAAGATTGTAAGGGATCCTGAGATCAAAAAGCTTGAGAAATTGCTG
CTGTATCACCATTTTACGTAAGTGCATCATATTCTGTTATATGTTTGTGTCATAGTATA
TGTTACCAATTTCTTTTAAATCACCTTTTACTTTATTGATAGTTTAAAAACGATTGTAAG
TGAAATTGCAATGGATGCTTTGTAATTCATTTCTCATTCTGGTCCAGTTACTTTGTA
[G,A]
GATAAATTTTGAAGAGTGGACATTGCTGAGTCTGAAGGTAACACACATTTTAACTGGGA
TACGATTGCTTTTGGAAACCTTAGACCCATTTTCACTCTTTTACTGACAGTGCTTGC
TTCTCCACATCCTCGCTCATTGAGGATCAGTCTTTGTAAGTCTCCTATTCTGCAGGT
GAAATTCCTTTTCAATTTCTGTCTTAGTCCATTTAGTGTGCTATAGTGAATATCTGAG
ACAGGGTAATTTATAAAGAAAAGACATTTATTTAGCTCACAGTTCCGAGGCTGGGAAGT (SEQ ID NO:43)

FIGURE 3-28

- 4113 CAGTTACTTTTCGTAGGATAAATTTTGGAGAGTGGACATTGCTGAGTCTGAAGGTAACACA
CATTTTAAACTGGGATACGTATTGCCTTTTCGGAACCTTAGACCCATTTTCACTCTTTTG
ACTGACAGTGCTTGCTTCTCCACATCCTCGCTCATTAGGGTATCAGTCTTTGTAAAGTC
TCCTATTCTGCAGGTGAAATTCCTTTTCATTCCTGTCTTAGTCCATTTAGTGTGCTAT
AGTGAATATCTGAGACAGGGTAATTTATAAAGAAAAGACATTTATTTAGCTCACAGTTC
[C,T]
GCAGGCTGGGAAGTTTAAGAAGCGTGGTCTGGCATCTGCTGGACTCCTGGGGAGGGCTT
TCCTGCTGTGTACAACATGGTGGAAAGTCAAAGTGGAAAGTGGACATGTGTGAAGAAGCA
AAATCCGAGGGGTGTCTGGCTTTATAGCAACCCAGCCTCGAGGGAAGTATCCATTACT
GAGGGAAGTAAATTCAGTCTCATGAGAGAGAGAACTCACTCACTACTGCAAGAATGACACC
AAGCCATTATGAGGGATCTGCCTCCGTAACCCCTGACACCTCCTGCTAGGTCCCTCCTCC (SEQ ID NO:44)
- 4337 CATTTAGTGTTGCTATAGTGGAATATCTGAGACAGGGTAATTTATAAAGAAAAGACATTT
ATTTAGCTCACAGTTCGCGAGGCTGGGAAGTTTAAGAAGCGTGGTCTGGCATCTGCTGG
ACTCCTGGGGAGGGCTTTCTGCTGTGTACAACATGGTGGAAAGTCAAAGTGGAAAGTGG
ACATGTGTGAAGAAGCAAAATCCGAGGGGTGTCTGGCTTTATAGCAACCCAGCCTCGAG
GGAAGTATCCATTACTGAGGGAAGTAAATTCAGTCTCATGAGAGAGAGAACTCACTCACT
[A,G]
CTGCAAGAATGACACCAAGCCATTATGAGGGATCTGCCTCCGTAACCCCTGACACCTCCT
GCTAGGTCCCTCCTCCCAACACGGCCACATCAGGGATCAGACTTCAACATGAGTTTTTGT
GGGGACAAACAAAACGTAGCACTTGCTTTGCCTTTTGGTTCTATTACATCCTCCACAGG
ATTGCATTATGCCTACCCATTTGGTGAGGGCAGTCTTCTTAATTGGTTTACTGATTCAA
ATGCTACCCTCCTCCAGAGACATCCTCACAGACACACCCAGAAATCATGTTTTACCAGTT (SEQ ID NO:45)
- 4473 TTCCTGCTGTGTACAACATGGTGGAAAGTCAAAGTGGAAAGTGGACATGTGTGAAGAAGC
AAAATCCGAGGGGTGTCTGGCTTTATAGCAACCCAGCCTCGAGGGAAGTATCCATTAC
TGAGGGAAGTAAATTCAGTCTCATGAGAGAGAGAACTCACTCACTACTGCAAGAATGACAC
CAAGCCATTATGAGGGATCTGCCTCCGTAACCCCTGACACCTCCTGCTAGGTCCCTCCTC
CCAACACGGCCACATCAGGGATCAGACTTCAACATGAGTTTTTGTGGGGACAAACAAAAC
[G,A]
TAGCACTTGCTTTGCCTTTTGGTTCTATTACATCCTCCACAGGATTGCATTATGCCTAC
CCATTTGGTGAGGGCAGTCTTCTTAATTGGTTTACTGATTCAAATGCTACCCTCCTCCA
GAGACATCCTCACAGACACACCCAGAAATCATGTTTTACCAGTTATCTGGGCATCCCTTA
GTCCAGACGAGTTGATACATAAAATTAACCATCACATGAGGATAGAATTAGGATTACAC
AGTCAACCTTTATGGGAGAAAATTTAGAGGCATGTGAGGGGTTATGTAATGTCAAGGA (SEQ ID NO:46)
- 6455 TGTTTATTGCATTGAGTGGAATCAGGATTTCACTCCATTAAGTAATTCCTCTGTAAACAA
AGAGGGTTTCATTTTATTTTATTTTATTTTATTTTCTGGAGAC
AGAATCTTGCTCTATCACCAGGCTGGAGTGCAGTGGTGCATCTCGGCTCACTGCAGCC
TCTGCTTCTGGATTCAAGCGATTCTTGTGCCTCAGCCTCCCAAGCAGCTGAGATTACAG
GCACATGCCACCACACCTGGTTAACTTTGTATTTCTAGTAGAGATGGGATTTTGCCAT
[T,G]
TTGGTCAGGCTGGTCTTGAATTCCTGGCCTCTAGTGATCTGCCTGCCTCTGCCTCTGAAA
GTGCTAAGATTACAGGCATGAGCTACCATGGCCAGCCCATTTCTTAATATTTTAAATTGT
CAGACATGTTATGGTTTCTGGCACAATATTAAGAAGACATGATATGAAATCACAGGGTGA
ATTTTAGGGCATCACACAGAAAGATTATGGTATAAGAAAAACAATGGAATTCAACTAC
ATTTCTGTCAAATGTTCTAAAAATATATAAAATCTGTATCTTTGTGTTCTCTCCTGATTT (SEQ ID NO:47)
- 6533 TTATTTTCAATTAATATTGCTTTTTTTTTTTTTTTTCTGGAGACAGAATCTTGCTCTATCAC
CAAGGCTGGAGTGCAGTGGTGCATCTCGGCTCACTGCAGCCTCTGCTTCTGGATTCAA
GCGATTCTTGTGCCTCAGCCTCCCAAGCAGCTGAGATTACAGGCACATGCCACCACACCT
GGTTAACTTTTGTATTTCTAGTAGAGATGGGATTTTGCCATGTTGGTCAAGGCTGGTCTT
GAATTCCTGGCCTCTAGTGATCTGCCTGCCTCTGCCTCTGAAAGTGCTAAGATTACAGGC
[T,G,A]
TGAGCTACCATGGCCAGCCCATTTCTTAATATTTTAAATTGTGAGACATGTTATGGTTTC
TGGCACAATATTAAGAAGACATGATATGAAATCACAGGGTGAATTTAGGGCATCACAAAC
AGAAAGATTATGGTATAAGAAAAACAATGGAATTCAACTACATTTCTGTCAAATGTTCT
AAAAATATATAAAATCTGTATCTTTGTGTTCTCTCCTGATTTATATTCTAAATTTGATGT

FIGURE 3-29

- TATCCTTCTCTGCAGAAATAAAGTGTCTGAAAGAATGAAAAAATGGAAGAATTCTTTAG (SEQ ID NO:48)
- 6919 ATGAAATCACAGGGTGAATTTTAGGGCATCACAAACAGAAAGATTATGGTATAAGAAAAAC
AATGGAATTCCTCACTACATTTCTGTCAAATGTTCTAAAAATATATAAAATCTGTATCTTT
GTGTTCTCTCCTGATTATATTCTAAATTTGATGTTATCCTTCTCTGCAGAAATAAAGTG
TCTGAAAGAATGAAAAAATGGAAGAATTTCTTAGTAAGGTATAAAATACCCTTTCTATC
TTTGTAGCATTCTAAGCCTTTTGTACCTTTCCAACTCCCAACATGCCATATTCCTGA
[G,C]
TAGGCCACAGCCATGTACATTGATCCCTTTATTTTCTTCTCTCTGCCTGAGATTTCTCTC
ATTCCTTCTCTGCTGGTATATGATTGCCATTGTTAAGGCCCACTCACCTTTA
TAATCTTCTAGCCCACTTTCTTTATCGGTATCCAGAAAAACAAAAGAAGCTTCACA
AGACAACATTCTGTAATACACTGCTTAACTTCTTTGACCCTGCTGAGTTCAAAAATCTT
ATCTTTTAAAGGATTGAATGGAGTCCACCAAGGTATCTATATTTGACAGGATTTATGAAA (SEQ ID NO:49)
- 7305 GATTGCCATTGTTTAAAGGCCCACTCACCTTTATAATCTTCTAGCCCACTTTCTTTA
TCGGTATTCAGAAAAACAAAAGAAGCTTCACAAGACAACATTCTGTAATACACTGCT
TAACTTCTTTGACCCTGCTGAGTTCAAAAATCTTATCTTTTAAAGGATTGAATGGAGTC
CACCAAGGTATCTATATTTGACAGGATTTATGAAAAACAAAAGGATTTGTTGAGAAAGTTT
GAAGCCTAACTCTGAAACGTGGATCATAGTGTTTACTACACATTAAGTGTTTAGTGGAT
[G,A]
TAATAGTTATTATTATAGGCTGTGGAATCAGAACAGGGTTCAAATGTTTTACCGCTTGC
TAGACTGTGGCCTTGGGCATGTTATTTAATGCCTGGAGGCCTCAAATGTTAACTAGGAAT
GGTAAGACCTACCCAGTAACTTAGCATAAATAGTAAATTCATTCAATTAATGTTTTCAA
CAGTGCCAGACATTGTTTAAATGAAGTGGGATATAGTGGTGAACAACACTGACAGCGTTC
TTCATTGTATTCTCAAAACCTCCCTATAGTAAGTAGGTCTGTGTGTGTGTAGGTGCA (SEQ ID NO:50)
- 7340 TAATCTTCTAGCCCACTTTCTTTATCGGTATTCAGAAAAACAAAAGAAGCTTCACA
AGACAACATTCTGTAATACACTGCTTAACTTCTTTGACCCTGCTGAGTTCAAAAATCTT
ATCTTTTAAAGGATTGAATGGAGTCCACCAAGGTATCTATATTTGACAGGATTTATGAAA
ACAAAAGGATTTGTTGAGAAAGTTGAAGCCTAACTCTGAAACGTGGATCATAGTGTTA
CTACACATTAAGTGTTTAGTGGATGTAATAGTTATTATTATAGGCTGTGGAATCAGAAC
[A,G]
GGGTTCAAATGTTTTACCGCTTGTCTAGACTGTGGCCTTGGGCATGTTATTTAATGCCTG
GAGGCCTCAAATGTTAACTAGGAATGGTAAGACCTACCCAGTAACTTAGCATAAATAGTA
AATTCATTCAATTAATGTTTTCAACAGTGCCAGACATTGTTTAAATGAAGTGGGATATA
GTGGTGAACAACACTGACAGCGTCTTCATTGTATTCTCAAAACCTCCCTATAGTAAGT
AGGTCTGTGTGTGTGTAGGTGCATGGGAATAAAAAATAATAAGCAAATAATGAACAG (SEQ ID NO:51)
- 7466 TTAAGGATTGAATGGAGTCCACCAAGGTATCTATATTTGACAGGATTTATGAAAAACAAA
GGATTTGTTGAGAAAGTTTGAAGCCTAACTCTGAAACGTGGATCATAGTGTTTACTACAC
ATTAAGTGTTTAGTGGATGTAATAGTTATTATTATAGGCTGTGGAATCAGAACAGGGTT
CAAATGTTTTACCGCTTGTCTAGACTGTGGCCTTGGGCATGTTATTTAATGCCTGGAGGC
CTCAAATGTTAACTAGGAATGGTAAGACCTACCCAGTAACTTAGCATAAATAGTAAATTC
[A,G]
TTCATTTAATGTTTTCAACAGTGCCAGACATTGTTTAAATGAAGTGGGATATAGTGGTG
AACAACTGACAGCGTCTTCATTGTATTCTCAAAACCTCCCTATAGTAAGTAGGTCT
GTGTGTGTGTAGGTGCATGGGAATAAAAAATAATAAGCAAATAATGAACAGGGTAAT
TTCAAAAAGCAGAAAGAGCTATTCAACAAAACCTACCTGCCTTTTATTAGATGAAACTCTC
AACTCTATGTTTGTCTCTCTCTGTCATTCTGTTAAATGCTGTCAGCCTGTTTCCCTTA (SEQ ID NO:52)
- 7589 AACTGTTTTAGTGGATGTAATAGTTATTATTATAGGCTGTGGAATCAGAACAGGGTTCAA
ATGTTTTACCGCTTGTCTAGACTGTGGCCTTGGGCATGTTATTTAATGCCTGGAGGCCTC
AAATGTTAACTAGGAATGGTAAGACCTACCCAGTAACTTAGCATAAATAGTAAATTCATT
CATTTAATGTTTTCAACAGTGCCAGACATTGTTTAAATGAAGTGGGATATAGTGGTGAA
CAACACTGACAGCGTCTTCATTGTATTCTCAAAACCTCCCTATAGTAAGTAGGTCTGT
[G,C]
TGTGTGTGTAGGTGCATGGGAATAAAAAATAATAAGCAAATAATGAACAGGGTAATTTT
AAAAAGCAGAAAGAGCTATTCAACAAAACCTACCTGCCTTTTATTAGATGAAACTCTCAAC

FIGURE 3-30

- TCTATGGTTTGTCTCTCCTGTCAATTCTGTTAAATGCTGTCAGCCTGTTTTCTTATCA
CCCTGGCCACGACTTCTGTCTTTCTGCTTGGTCTGTAGACTCTAACCCAAGGCTCATT
CTCTGCCTGGCTATCTGCCTTCTGTGGCTCTTTGCCACTACCTACATTTTCTGTGTTGCA (SEQ ID NO: 53)
- 7810 CTGGGGATATAGTGGTGAACAACACTGACAGCGTTCTTCATTGTATTCTCAAAACCTCC
CTATAGTAAGTAGGTCTGTGTGTGTGTGTAGGTGCATGGGAATAAAAAATAAGCAA
ATAATGAACAGGGTAATTTCAAAAAGCAGAAAGAGCTATTCAACAAACTACCTGCCCTT
TATTAGATGAACTCTCAACTCTATGGTTTGTCTCTCCTGTCAATTCTGTTAAATGCTG
TCAGCCTGTTTTCTTATCACCTGGCCACGACTTCTGTCTTTCTGCTTGGTCTGTAG
[A,C]
CTCTAACCCAAGGCTCATTCTCTGCCTGGCTATCTGCCTTCTGTGGCTCTTTGCCACTAC
CTACATTTTCTGTGTGACAGGGAAGGACCATTCCCTGTGGACCATAAAATTCTCTTTT
TGAAAGAATTCTTCTGATTGGGCCACAGCACATCTTGTGAAACAGCATTAGACATTTG
CCTGCTCAGCAGCTCTGGGGGAAAATGTTTACTGAGAAGCGTACAGTAGTTTTTTGA
CTAACCATGGTGCAACCTCTCCAGAGGGAACTATGAGTATTTCAAGGACATGTGAT (SEQ ID NO: 54)
- 9104 TTAACGAATTATTGTAGAAACAGAAAAACAATACTGTGTTCTCATTTACAGGGGAGC
TAAACCTTGGGTAAATGGGCATAAAGATGGGAACAATAGACACTAGGGACTCCAAAGG
GGGAGGGAGGGAGGAGGGCAAGGGCTGGAAAGCTTCTCTACTGGGTACTTTGTTACAAC
CTGGGTGATGGCAGATTAGGAGCTCAAACCCAGTATCACACAGTATACCTTGTAAAC
AGCTGATGGTGAACCCCTGAATCTACAATAAAATTATTTTATTTAAAAAATCATTATA
[G,A]
GGATTTTTAAAAAGAAGGATTCTAGACAGGTGCAGCCAACAATTTTTTTAAATGTTG
GCAGGCCGCCACCGCCAGTCACTTATGCTGCAATAGCCCATGTCCCAACATTCCCAACCT
ACTTCTCTCCAAAAGAGAAGCTATACTTTAGATGGCCCTGTGCTGGGTTCTCCCTGGAA
GTTTCTGGGGAAAGGGGCTTGAGTTGCCCGACTGGAAGTCTTCTGGAGTGGGAGCCGGG
GCTTCTGATCAGACGTGAGTGAGGCAGGAAGTCCGCGTCTCCAGCGCAGCCAGAGTG (SEQ ID NO: 55)
- 9503 CATGTCCCAACATTCCCAACCTACTTCTCTCCAAAAGAGAAGCTATACTTTAGATGGCC
CTGTGCTGGGTTCTCCCTGGAGTTTCTGGGGAAAGGGGCTTGAGTTGCCCGACTGGAC
TCTTCTGGAGTGGGAGCCGGGCTTCTGATCAGACGTGAGTGAGGCAGGAAGTCCGCGG
TCTCCAGCGCAGCCAGAGTGCGGTCCACGCAGGTCCCGGTCTGCGCGCTCGCGCC
TTTGCGCTGAAGCCGTTAGGATGAGCCCTCTCCTTCCAGAGCTTTAACCGATGAAGGTGC
[A,T]
TTGTGTTTGGCGCCCCTGAGGAGGATGCTGTCTTAGGCCTCTTCCACTGGACGTGTGTG
GTGGGCAGAGATCCCGTTCTGTCGGTGCCTTCCACCCGCTGGGGCTCACTCAGGCCGC
GGAGCTGCGAGGGAGACATCCTCGATGGACTCCCTTACGGAGATCTCTTTGGTACCTG
GACTATAACAAGGATGGGACCTTGACATTTTGGAGTTCAGGAAGGCCTGGAGGATGTA
GGGGCCATTCAATCTCTAGAGGAAGCGAAGGTGGGTCTCACTGGGGCTGTAATCAGAGAG (SEQ ID NO: 56)
- 9898 ACCCGCTGGGGCTCACTCAGGCCGCGGAGCTGCGAGGGAGACATCCTCGATGGACTCCC
TCTACGGAGATCTCTTTTGGTACCTGGACTATAACAAGGATGGGACCTTGGACATTTTGG
AGCTTCAGGAAGGCCTGGAGGATGTAGGGGCCATTCAATCTCTAGAGGAAGCGAAGGTGG
GTCTCACTGGGGCTGTAATCAGAGAGACGTTGGGGCTGGGAGCCCTGGAGAGGCATTGGG
CAGAGAGGGCAAAATTTACATGTTGTCAAGCTTGACCTGGGCCACTGCAGTGTTCAAGT
[G,C]
GTTGACCAGCGTTACCGTTTATTAAGAATAACAACACAGCTAACACATTTCTCAAGTATT
TTTCTCCGTTTTCTCCTTGGCTGTAGTAAAATCTCCAACCTCAGATTGCTCTCAAGATGT
TGGCTACATACAGCCTTGTCTTAGGAGTCACCTTGTTCAATGTGCTCACCTGTCATTAGT
CACCCAGAGGGGCGTCTAGGCTAAAGATGCGCCCTCCCCAGTTCAGAGAACTGGAATAAT
CACTCTACGTGTATTTGGGAGTGGGGTGGTGATTGGAAATTTCTGATGTTATGTTTTGG (SEQ ID NO: 57)
- 10196 GTGGTTGACCAGCGTTACCGTTTATTAAGAATAACAACACAGCTAACACATTTCTCAAGT
ATTTTCTCCGTTTTCTCCTTGGCTGTAGTAAAATCTCCAACCTCAGATTGCTCTCAAGA
TGTTGGCTACATACAGCCTTGTCTTAGGAGTCACCTTGTTCAATGTGCTCACCTGTCATT
AGTCACCAGAGGGGCGTCTAGGCTAAAGATGCGCCCTCCCCAGTTCAGAGAACTGGAAT
AATCACTCTACGTGTATTTGGGAGTGGGGTGGTGATTGGAAATTTCTGATGTTATGTTTT
[T,C]

FIGURE 3-31

GGTTTCTGTTCTCTGGAAGGGGGCAGTGGAAGTGGCTTTTACTCTCGGGTTTCACTAGTGC
TGAGGTTTCTCCTATAATATGCCTTAATTGATAGACCCTAGTTATCAGTACCGAGCTTAGG
CTAACCTTCTCTTCCCCAGAAGGCTAACCTACAGGCTCCTTCTCAGCATGTTGTGCTTC
GTACATACTCCTATTGCAGTATTTCCAAGTCATTTTTCATTTGGAATTTATTATTGTATA
TAATAATTACTTTATAAGTATATTTGCTCTTTGGATGTTTGACCCGGTAGACTGGGAGAT

(SEQ ID NO:58)

12327 GTCATGTTATTTAATGCCTGGAGGCCCTCAAATGTTAACTAGGTAATGGTAAGACCTACCC
AGTAACTTAGCATAAATAGTAAATTCATTCATTTAATGTTTTCAAACAGTGCCAGACATT
GTTTAATGAACTGGGGATATAGTGGTGAACAACACTGACAGCGTTCTTCATTGTATTCTC
AAAACCTCCCTATAGTAAGTAGGTCTGTGTGTGTGTAGGTGCATGGGGAATAAAAAA
TAATAAGCAAATAATGAACAATAAAATTATTTTATTTAAAAAAGAAATGATACTTAC
[C,G,A]
TTGTCGTGTTAAGATACAAAAGCAATAACTTTTTATTGTGAAAAATAGTCTGTTTTTGAAC
AATATATTGTTTTGTTTTTCTGTGAAAGTTGAGAACTAAATATACGAAGAGATAATG
GTCAGACCATAAATAAAATAGAACTTTGACTCAAAATTTACAGCAGTCTGCCAGAAAA
CCAGCCCTTTATCTAAAAATAACAGACCAGGAAACCAGCCTGTTATGTCAGACTTATAGG
AAGTCAGGTTGCTATCTCTAGAGACAATACACAAAGCTATGCAATAACTGCTGTAAACAGC

(SEQ ID NO:59)

13749 TACAGGCGTGAGCCACCATGCGCCAGCCATAGACTATATATTTTTGATCTGATAACTGG
TTCAGCTACTAAGTGACTAACAGGCAAGTAGCATCTATAGTGTGGATATGCTGGACAAAA
GGACATTCACCTCCTGGGCAGGATGGCAGAGAATGTTGAGAGATTTTATCATGCTACTCA
GAATGGTGTGCAATTTAAACTTATGAGTTGTTTGTCTGGAGTTTCCATTTAATAGT
TCAGACCATGGATTGACCGCAGGTAAGTAACTGAACTGTGGAGAGTGAACTGTGGATAAGGG
[G,A]
GGACTATTGTATTGTTAAGTCAGACTCATTAGGCAATCATAACTCTTGATTTGCCATCAG
AAATGCTGCAGAAATATGGGTTAAAAAACTGTTCAAAATAGGGTCAGGGATGTCCTT
TAACCTGTTACTTCCAAAATGTTAGTGAAAAGTGTGGCCCCAAAGAGTGAAAGGAACAAA
TGACTAAGAGAAAATCTTGTTTTAGGATGACAGATTAAGAAAGCAACTTGCTGAAA
CACTGAAAATCTCTCACTTGTAAAGATAACACAAAAGTGGCTAAAAGTGGTTGGAATGAA

(SEQ ID NO:60)

14150 ATAGGGTCAGGGATGTCCTTTAACTTGTTACTTCCAAAATGTTAGTGAAAAGTGTGGCCC
CAAAGAGTGAAAGGAACAAATGACTAAGAGAAAATCTTGTTTTAGGATGACAGATTAAA
AAAGAAGCAACTTGCTGAAACACTGAAAATCTCTCACTTGTAAAGATAACACAAAAGTGG
CTAAAAGTGGTTGGAATGAATATGGCCAACTCAAGTCTGCACAGAACTAACTGGTGATG
TTACAGCCCAAATTTCCACCACATATTTATACTAACTCCCCCGGATTTTCACACATGA
[T,C]
CTGTGAGGTAGCATGAAGAGGTAAGTATGCATGCCTAAGGACTTGGGAGACCTCCCCATT
TCCTTCCACCAATCACCCTAATCCAGAAATCCGCCCCAAACCTTTTCTAATAACTAC
CTTAAAGCCAGCATAGGGAGACAGATTTGAGCTGGACTCCTGTCTTCTGTGGGTACCT
TGCAATAAAAAGCTTTTCTTTCTCAACACCTGGTATTATAGTATTGACTTCTAGTTTCT
CGGCAGCAAGCCCCCTTTGGTGGTGACTATTTCTGTTGCTGATATTTCCATTGGCCA

(SEQ ID NO:61)

14529 ACTAATCCCAGAATCCGCCCCAAACCTTTTCTAATAACTACCTTAAAGCCAGCATAGGG
AGACAGATTTGAGCTGGACTCCTGTCTTCTGTGGGTACCTTGCAATAAAAAGCTTTTC
TTTTCTCAACACCTGGTATTATAGTATTGACTTCTAGTTTCATCGGGCAGCAAGCCCCCTT
TGGTCGGTGACTATTTCTGTTGCTGATATTTCCATTGGCCAAATATAAACCTCTTGA
TGAAACTTCAGTACGTAATGGCGCCACAGAATGCTGTGACATTTTCTCTTGATTATA
[G,A]
CAGGTTACTTTACTGAATACCGTAGGCAGTTATAACACACTAAGTATTTGTGTATCTAAA
CATAGAAAAGATACAGTAAAAATATGGTAATTTTTTCAACTTTTAGTTGAGATTTGGAG
GGTATGTGCATTTGTTACAAGGGTATATTGCATGATGCTGAGGTTGGGGTACAATTG
AACCTGTCAACCAGGTAGTGAGCATAGTACCAATCGATAATTTTCAACCCTTGCCA
TTCCCTCCCCGTTCTTGTAAGTCCCCAGTTTCTGCTTTCCCATCTTATATCCGTGTGCA

(SEQ ID NO:62)

14653 CTCAACACCTGGTATTATAGTATTGACTTCTAGTTTCATCGGGCAGCAAGCCCCCTTTGGT
CGGTGACTATTTCTGTTGCTGATATTTCCATTGGCCAAATATAAACCTCTTAGATGAA
ACTTCAGTACGTAATGGCGCCACAGAATGCTGTGACATTTTCTCTTGATTATAGCAG
GTTACTTTACTGAATACCGTAGGCAGTTATAACACACTAAGTATTTGTGTATCTAAACAT

FIGURE 3-32



AGAAAAGATACAGTAAAAATATGGTAATTTTTTTCAACTTTTAGTTGAGATTTGGAGGGT
[G,A]
TGTGCACATTTGTTACAAGGGTATATTGCATGATGCTGAGGTTTGGGGTACAATTGAACC
CTGTACCCAGGTAGTGAGCATAGTACCCAATCGATAATTTTTCAACCCTTGCCATTCC
CTCCCCGTTCTTGTAGTCCCAAGTTCTGCTTTCCCATCTTTATATCCGTGTGCACCCC
ATGTTTTGCTCCCATGTGTATGTGAGAACTTGTGGTGTTTGGTTTTCTATTTCTGCGTTG
ATTCGCTTAGGATAATGGCCTTCAGCTGCATCCATGTTGCTGCAGAGGACGTGATTTTAT

(SEQ ID NO:63)

15871 AGGAGTTTATCAATTTTATTAGTCTTTTCAAAGAACCATCTTTGGCTTTGTTAATCCTC
CCAATGGTGTGTTTTCTTTCTATTACTTTTGCTCTTTATTTCTTCAACTTCTTTTTT
GCTTAATTTTAAAATAATTTCTTGAGATTGAGATAAGCCTCAATGATGGGTACCGATTT
CCAGTCTTTCTTTCTTTCTAATTATGCATTTTAAACCAGAAATCTTTCTCTAAGTGTAGC
TTTAGTTGCAGCTCACAAGTTTCAGATCTGTCTCTCAGTCTGGAGGTTGGAGATCTGACC
[A,G]
TGACCATGAAACCATCCAGTCACAATGTGGCATTATTTTTTTAATTTTTTTTTTTTTTTT
TGAGATAGAGTTTCACTCTTATTGCCTAGGCTGGTGTGCAATGGTGCGATCTCGGCTCAC
AGCAACCTCCACCTCCAGGTTCAAGCGATTCTTTGCTCAGCCTCCAAGTAGCTGGG
ATTACAGGCATGCGCCACCATGCCCAACTAATTTGTATTTTAGTAGAGATGGGGGTTT
TCCATGTTGGTCAGGTTGGTCTTGAACCTCCGACCTCAGGTGATCCGCCACCTCAGCCT

(SEQ ID NO:64)

19244 GTGGCATTATTGGTTCATATTTTTATTTTTAGACTTCCTTAATGCAAAACATACAGT
TGATCCTCATTATTTGGGGATTCTGTATTTGCAAATTTGCCTACTCAATAAAATTTATCC
CCAAAGTAACCCCAAAATATATACTCACAGTACTTTCCAGGCATTATGGACATGCACA
GAGCAGTGAAAAACTTGAGTTGCTCAGCATGTACATTCCTAGCTAGTAGAATAAGGCAAT
ACTCTGCCTTCTTGTTTCAGCTCTCATACTATTAAGTAGCAAGTATCCCTTTCAAGGTCT
[G,A]
TTTTGTGCCAGTTTTTGCATTTTTGTATTTTGTGGTAATTTCTTTTTAAATGTTCC
CCAAAGGTAGTGCTGAAGTGCTGTCTAGTGTTCTAAGTGCAAGAAAGCCATAGCATGCC
TTATGGAGAAAATATATGCGTTGGATAAGCTTTGCCCAAATTCATGTTAGTGAATCAA
CAGCACACATTAATGAGGTGCCTTCAAACAGAAACAGACATAAGACATGGTTATGTATT
AATCAGTTGATGAAAGTGTTGTAATCAGAGGCTCACAGGAACCTAACCCCTGTTTTCTCTG

(SEQ ID NO:65)

19387 CTCACAGTACTTTCCAGGCATTATGGACATGCACAGAGCAGTGAAAACTTGAGTTGC
TCAGCATGTACATTCCTAGCTAGTAGAATAAGGCAATACTCTGCCTTCTTGTTTCAGCTC
TCATACTATTAAGTAGCAAGTATCCCTTTCAAGGTCTATTTTGTGCCAGTTTTTGCAATTT
TTGTATTTTTGTTGGTAATTTCTTTTTAAATGTTCCCAAAGGTAGTGCTGAAGTGCT
GTCTAGTGTTCTAAGTGCAAGAAAGCCATAGCATGCCTTATGGAGAAAATATATGCGTT
[T,G]
GATAAGCTTTGCCCAAATTCATGTTAGTGAATCAACAGCACACATTAAATGAGGTGCC
TTCAAACAGAAACAGACATAAGACATGGTTATGTATTAATCAGTTGATGAAAGTGTTGTA
ATCAGAGGCTCACAGGAACCTAACCCCTGTTTTCTGTAGGAACAATGGTTTGGTATTTG
CTAATTCAGTGTTTGCAATGAATATAGAATTTATGGAAGATGATTGCTGTGAATAATGA
GAATTAACCATATCTCTTTAAGAGTGCAATTTCTAAAGGAGAATATTCAGAAGGGTATTTG

(SEQ ID NO:66)

19447 TCAGCATGTACATTCCTAGCTAGTAGAATAAGGCAATACTCTGCCTTCTTGTTTCAGCTC
TCATACTATTAAGTAGCAAGTATCCCTTTCAAGGTCTATTTTGTGCCAGTTTTTGCAATTT
TTGTATTTTTGTTGGTAATTTCTTTTTAAATGTTCCCAAAGGTAGTGCTGAAGTGCT
GTCTAGTGTTCTAAGTGCAAGAAAGCCATAGCATGCCTTATGGAGAAAATATATGCGTT
GGATAAGCTTTGCCCAAATTCATGTTAGTGAATCAACAGCACACATTAAATGAGGTGC
[C,G]
TTCAAACAGAAACAGACATAAGACATGGTTATGTATTAATCAGTTGATGAAAGTGTTGTA
ATCAGAGGCTCACAGGAACCTAACCCCTGTTTTCTGTAGGAACAATGGTTTGGTATTTG
CTAATTCAGTGTTTGCAATGAATATAGAATTTATGGAAGATGATTGCTGTGAATAATGA
GAATTAACCATATCTCTTTAAGAGTGCAATTTCTAAAGGAGAATATTCAGAAGGGTATTTG
CATAATTTCTTTACTAACAGATGCTGCCTCTCACTGTCTTACATGGTCCAGATTCTCAT

(SEQ ID NO:67)

20076 TCTCTCAGAACTCTGTCTCTCCTCCAGGGTCTTTCTCCAAGAAAGTCTATCCTTTTAC
CACTAACAGTAATTTGGTCTTCTCTTTTCTGGAGAAGTCAGCTGTTTATGCTGCTTC

FIGURE 3-33

(SEQ ID NO:68)

(SEQ ID NO:69)

(SEQ ID NO:70)

(SEQ ID NO:71)

(SEQ ID NO:72)

FIGURE 3-34

- 21701 CATTGATTCAAACCTAAGAAGACTAGCAGATTATCATCATTTATTTAACCTAGATGTGACTG
GAAAAAGGGAAATTACTAAGCTCTCCAAGCTAACAAAGAAATACCTGTTTAACTTTCA
GAAAAAGAAATGCAATTTGAACCTTATTGTCTGGGGCAATCAGTTTGACTATTTAAGT
CAGACTTTTATACTCTTAATGTTTTGTTTCATGGGATAGAGCAGTAATCTCTGCAGCCCA
GGTGCTCTCAAACTCTGTTGCTATAAACACAGGGCAGGAAGTATTTTTATGATAAC
[G,A]
TAAAAACAGAAAAGGACAATTATATTGTATTAATATTGTTGTGAATATTTTCAGTCCTCAC
ATTGTCTAAAAATCTTTCTAAATGGCTTTGTTATTGAATTTATCTCATTTTATATCTGTG
CCAACAGCATTTTCATCCTTTCTCTTCATAATTTCTTTTACAAACAGCTGCTCAAGAGGA
AGGCTCAAAGTCTCAAGGCTGAGCACGTAATGACTTTTGTTAGTACTAGATGAGAAGGGC
TTTCCTGAGGAAATGAAAACCTAAAACATGAAAAGAAGATAAACAGAATTTGGACAGTGA (SEQ ID NO:73)
- 21710 AAACCTAAGAAGACTAGCAGATTATCATCATTTATTTAACCTAGATGTGACTGGAAAAAGG
GAAATTTACTAAGCTCTCCAAGCTAACAAAGAAATACCTGTTTAACTTTTCAGAAAAACAGA
AATGCAAAATTTGAACCTTATTGTCTGGGGCAATCAGTTTGACTATTTAAGTCAGACTTTT
ATACTCTTAATGTTTTGTTTCATGGGATAGAGCAGTAATCTCTGCAGCCAGGTGCTCTC
AAATACTCTGTTGCTATAAACACAGGGCAGGAAGTATTTTTATGATAACGTAAAAACAG
[A,-]
AAAGGACAATTATATTGTATTAATATTGTTGTGAATATTTTCAGTCCTCACATTGTCTAA
AAATCTTTCTAAATGGCTTTGTTATTGAATTTATCTCATTTTATATCTGTGCCAACAGCA
TTTTCATCCTTTCTCTTCATAATTTCTTTTACAAACAGCTGCTCAAGAGGAAGGCTCAAA
GTCTCAAGGCTGAGCACGTAATGACTTTTGTTAGTACTAGATGAGAAGGGCTTTCTGAG
GAAATGAAAACCTAAAACATGAAAAGAAGATAAACAGAATTTGGACAGTGAGATATAGAG (SEQ ID NO:74)
- 21826 CAGAAATGCAAAATTTGAACCTTATTGTCTGGGGCAATCAGTTTGACTATTTAAGTCAGAC
TTTTATACTCTTAATGTTTGTGTTTCATGGGATAGAGCAGTAATCTCTGCAGCCAGGTGC
TCTCAAATACTCTGTTGCTATAAACACAGGGCAGGAAGTATTTTTATGATAACGTAAA
ACAGAAAAGGACAATTATATTGTATTAATATTGTTGTGAATATTTTCAGTCCTCACATTG
TCTAAAAATCTTTCTAAATGGCTTTGTTATTGAATTTATCTCATTTTATATCTGTGCCAA
[C,T]
AGCATTTTTCATCCTTTCTCTTCATAATTTCTTTTACAAACAGCTGCTCAAGAGGAAGGCT
CAAAGTCTCAAGGCTGAGCACGTAATGACTTTTGTTAGTACTAGATGAGAAGGGCTTTCC
TGAGGAAATGAAAACCTAAAACATGAAAAGAAGATAAACAGAATTTGGACAGTGAGATAT
AGAGCATATAATATTCTGCTTCTAAAGTAATATTCTTCTAGGAAAGTGAGGGCGTTTCCC
TGGCTGTTAGGCCAGAAATCATATTCCTATATTTTCTTTGATAGCTTTAGGAATAATGCA (SEQ ID NO:75)
- 21840 TGAACCTTATTGTCTGGGGCAATCAGTTTGACTATTTAAGTCAGACTTTTATACTCTTAA
TGTTTTGTTTCATGGGATAGAGCAGTAATCTCTGCAGCCAGGTGCTCTCAAATACTCTG
TTGCTATAAACACAGGGCAGGAAGTATTTTTATGATAACGTAAAACAGAAAAGGACAA
TTATATTGTATTAATATTGTTGTGAATATTTTCAGTCCTCACATTGTCTAAAAATCTTTC
TAAATGGCTTTGTTATTGAATTTATCTCATTTTATATCTGTGCCAACAGCATTTTCATCC
[-,T]
TTCTCTTCATAATTTCTTTTACAAACAGCTGCTCAAGAGGAAGGCTCAAAGTCTCAAGGC
TGAGCACGTAATGACTTTTGTTAGTACTAGATGAGAAGGGCTTTCTGAGGAAATGAAAA
CCTAAAACATGAAAAGAAGATAAACAGAATTTGGACAGTGAGATATAGAGCATATAATAT
TCTGCTTCTAAAGTAATATTCTTCTAGGAAAGTGAGGGCGTTTCCCTGGCTGTTAGGCCA
GAAATCATATTCCTATATTTTCTTTGATAGCTTTAGGAATAATGCAAATCTAAGCCCAA (SEQ ID NO:76)
- 21841 GAACCTTATTGTCTGGGGCAATCAGTTTGACTATTTAAGTCAGACTTTTATACTCTTAAT
GTTTTGTTTCATGGGATAGAGCAGTAATCTCTGCAGCCAGGTGCTCTCAAATACTCTGT
TGCTATAAACACAGGGCAGGAAGTATTTTTATGATAACGTAAAACAGAAAAGGACAA
TATATTGTATTAATATTGTTGTGAATATTTTCAGTCCTCACATTGTCTAAAAATCTTTC
AAATGGCTTTGTTATTGAATTTATCTCATTTTATATCTGTGCCAACAGCATTTTCATCCT
[-,C,T]
TCTCTTCATAATTTCTTTTACAAACAGCTGCTCAAGAGGAAGGCTCAAAGTCTCAAGGCT
GAGCACGTAATGACTTTTGTTAGTACTAGATGAGAAGGGCTTTCTGAGGAAATGAAAAC
CTAAAACATGAAAAGAAGATAAACAGAATTTGGACAGTGAGATATAGAGCATATAATATT
CTGCTTCTAAAGTAATATTCTTCTAGGAAAGTGAGGGCGTTTCCCTGGCTGTTAGGCCAG

FIGURE 3-35

- AAATCATATTCCTATATTTTCTTTGATAGCTTTAGGAATAATGCAAATTCTAAGCCCAAG (SEQ ID NO:77)
- 21843 ACCTTATTGTCTGGGGCAATCAGTTTGACTATTTAAGTCAGACTTTTATACTCTTAATGT
TTTGTTCATGGGATAGAGCAGTAATCTCTGCAGCCAGGTGCTCTCAAATACTCTGTTG
CTATAAACACAGGGCAGGAACTGATTTTATGATAACGTAACAGAAAAGGACAATTA
TATTGTATTAATATTGTTGTGAATATTTTCAGTCCTCACATTGTCTAAAAATCTTTCTAA
ATGGCTTTGTTATTGAATTTATCTCATTTTATATCTGTGCCAACAGCATTTTCATCCTTT
[-,C]
TCTTCATAATTTCTTTTACAAACAGCTGCTCAAGAGGAAGGCTCAAAGTCTCAAGGCTGA
GCACGTAATGACTTTTGTAGTACTAGATGAGAAGGGCTTTCTGAGGAAATGAAAACCT
AAAACATGAAAAGAAGATAAACAGAATTTGGACAGTGAGATATAGAGCATATAATATTCT
GCTTCTAAAGTAATATTCTTCTAGGAAAGTGAGGGCGTTCCCTGGCTGTTAGGCCAGAA
ATCATATTCCTATATTTTCTTTGATAGCTTTAGGAATAATGCAAATTCTAAGCCCAAGCT (SEQ ID NO:78)
- 22045 ATATTTTCAGTCCTCACATTGTCTAAAAATCTTTCTAAATGGCTTTGTTATTGAATTTAT
CTCATTTTATATCTGTGCCAACAGCATTTTCATCCTTTCTCTTCATAATTTCTTTTACAA
ACAGCTGCTCAAGAGGAAGGCTCAAAGTCTCAAGGCTGAGCACGTAATGACTTTTGTAG
TACTAGATGAGAAGGGCTTTCTGAGGAAATGAAAACCTAAAACATGAAAAGAAGATAAAA
CAGAATTTGGACAGTGAGATATAGAGCATATAATATTCTGCTTCTAAAGTAATATTCTTC
[C,A,T]
AGGAAAGTGAGGGCGTTTCCCTGGCTGTTAGGCCAGAAATCATATTCCTATATTTTCTTT
GATAGCTTTAGGAATAATGCAAATTCTAAGCCCAAGCTTCAGAATAGACTAAGAAGTATT
AGCTTAGCTGCCATGACAAAATACCATAGGCTGGATGCATTAACAATGGAAATTTAGTT
TTTCACAGGTCTGGGAGCTGGGAAGTTTAAGATGAGAGTGCCAGCATGGTTGGGTTGTAG
TGAGGGCTCTCTTTCTGGCTTGAGATAGACCCCTTCTCACTGTATTGTCATATGGCAGA (SEQ ID NO:79)
- 22061 CATTGTCTAAAAATCTTTCTAAATGGCTTTGTTATTGAATTTATCTCATTTTATATCTGT
GCCAACAGCATTTTCATCCTTTCTCTTCATAATTTCTTTTACAAACAGCTGCTCAAGAGG
AAGGCTCAAAGTCTCAAGGCTGAGCACGTAATGACTTTTGTAGTACTAGATGAGAAGGG
CTTTCTGAGGAAATGAAAACCTAAAACATGAAAAGAAGATAAACAGAATTTGGACAGTG
AGATATAGAGCATATAATATTCTGCTTCTAAAGTAATATTCTTCTAGGAAAGTGAGGGCG
[G,T]
TTCCCTGGCTGTTAGGCCAGAAATCATATTCCTATATTTTCTTTGATAGCTTTAGGAATA
ATGCAAATTCTAAGCCCAAGCTTCAGAATAGACTAAGAAGTATTAGCTTAGCTGCCATGA
CAAAATACCATAGGCTGGATGCATTAACAATGGAAATTTAGTTTTTCACAGGTCTGGGA
GCTGGGAAGTTTAAGATGAGAGTGCCAGCATGGTTGGGTTGTAGTGAGGGCTCTCTTTCT
GGCTTGAGATAGACCCCTTCTCACTGTATTGTCATATGGCAGAGAGAGAGAGAGAGAGA (SEQ ID NO:80)
- 22348 GAAAGTGAGGGCGTTTCCCTGGCTGTTAGGCCAGAAATCATATTCCTATATTTTCTTTGA
TAGCTTTAGGAATAATGCAAATTCTAAGCCCAAGCTTCAGAATAGACTAAGAAGTATTAG
CTTAGCTGCCATGACAAAATACCATAGGCTGGATGCATTAACAATGGAAATTTAGTTT
TCACAGGTCTGGGAGCTGGGAAGTTTAAGATGAGAGTGCCAGCATGGTTGGGTTGTAGTG
AGGGCTCTCTTTCTGGCTTGAGATAGACCCCTTCTCACTGTATTGTCATATGGCAGAGA
[-,A,G]
AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGGGATCTTTCTCTTGCTTTCTATTATAAGG
CCATAGTCCTGTTGGATCAGGGTTCCATTCTTATGACTTTATTTGACTTTACCCCCCTAA
GATGCTATCTCCAGATATAATCACACGGTGGGTTAGGGCTCAACATTTGGATTTGGGAG
GGACACAGCTCAGTCCATAGCAAAGGATAATGCAGAGGGTTGGATATTTAAAAGTAGCTA
CACAAATTTTAAATATAAATATTTTATGGTAACTTTTTTTTTTTTTTTGGATGGAGTCTAG (SEQ ID NO:81)
- 22682 ATCTTTCTCTTGCTTTCTATTATAAGGCCATAGTCCTGTTGGATCAGGGTTCATTCTTA
TGACTTTATTTGACTTTACCCCCCTAAGATGCTATCTCCAGATATAATCACACGGTGGGT
TAGGGCTCAACATTTGGATTTGGGAGGGACACAGCTCAGTCCATAGCAAAGGATAATGC
AGAGGGTTGGATATTTAAAAGTAGCTACACAATTTTAAATATAAATATTTTATGGTAAC
TTTTTTTTTTTTTGGATGGAGTCTAGCTCTGTTGCCAGGCTGGAGCGCAATGGTGCGA
[A,G,T]
CTCAGCTCACTGCAACCTCCGCCTCCAGGTTCAAGCAATTCCTGCCTCAGCCTCCTG
AGTAGTTGGGACTATAGGCACGCGCCACCACGCCTGGCTATTTTTTTTTTTTATTTTACTA

FIGURE 3-36

GAGACGGGTTTGCACCATATTGGTCAGGCTTGTCTCGAACTCCTGACATCAGGTGATCCA
CCCATCTTGGCCTCCCAAAGTGCTGGGATTACAGAAGTGAGCCACCGCGCTAGCCAGCA
GCTTTACTGAGATGTAATTCACATGCCATAAATTCACITTTCTAAAGTATACAATTCAGT

(SEQ ID NO:82)

22783

ATATAATCACACGGTGGGTTAGGGCCTCAACATTTGGATTTGGGAGGGACACAGCTCAGT
CCATAGCAAAGGATAATGCAGAGGGTTGGATATTTAAAAGTAGCTACACAATTTTAAATA
TAAATATTTTATGGTAACITTTTTTTTTTTTGGAGATGGAGTCTAGCTCTGTTGCCAGG
CTGGAGCGCAATGGTGGATCTCAGCTCACTGCAACCTCCGCTCCCAGGTTCAAGCAAT
TCTCTGCCTCAGCCTCCTGAGTAGTTGGGACTATAGGCACGCGCCACCACGCTGGCTA
[-,T]

TTTTTTTTTATTTTTACTAGAGACGGGTTTGCACCATATTGGTCAGGCTTGTCTCGAACT
CCTGACATCAGGTGATCCACCATCTTGGCCTCCCAAAGTGCTGGGATTACAGAAGTGAG
CCACCGCGCTAGCCAGCAGCTTTACTGAGATGTAATTCACATGCCATAAATTCACITTT
CTAAAGTATACAATTCAGTGACTTAAACATTTATTTATTTTAAATTGACAGAATTACA
TGATTTATCATGTACAACATGATGTTTTGAAGTATATGTACATTGTGGAGTGACTAAGT

(SEQ ID NO:83)

23448

TTCTCTTAGTATTTTTCAAGAATATAATATATTATTATTAATTGTAGTCTTCATGTTGTA
TAGTGGAGCTCTTGAACITATTCCTCATGTCAAGCTGAAATTGTGTCTTTAACACAA
ACCATACCCGACTCCCAAAGTATTCGTCTCTGCTTCTATGAGATTAACITTTCTGAT
TCCACATGAGTGAGATCATGCAGTATTTATTTGTCTTTACCTGGCTATTTTCATTCATAT
TGTTACAGATAACAGGATTCCTTCTTTTTTAATGGCCGAATAGTTTCTATTGTATAT
[A,G]

TATAGCACATTTTCTCTCTTCATGCATTGGTGGACACTTAGGTTGATTCCGTATCTTGGC
TATCGTGAATAGTGCTATAATGAACATGGGAATGCACATGGCTCTTTGACATATTGATTT
CATTTTATATATGTGTATATATATGTATACACACACATACATACAGTGGTGGGATTGC
AGGATCATATGGTAGTTCTATATTTAATTTTAAAGGAACTCCATACTGCTTCCATAAT
GGCTGTATTAGTTAACTCCTCACCAACAGGCTGCAAAAGTTCCTTTTCTCTACATACT

(SEQ ID NO:84)

24960

TTTGTCTAGAGTATAGTTTAAAGTCTGATGTTTCTTACTGATTTTCTGTTGAGATGATTT
GTCTATTGCTGAAGGTAGGGTGTGAAGTCCCCTACTATTGCTGTATTGCAGTCTCTCTC
TCCTTTGAGACGTATTAATGGTTTTTATTTTATTTTATTTGTTGTTGTTGTTGTTGTTG
TGTGTTTTTGGAGACGGAGTCTCACTCTGTACCAGGCTGGAGTGCAGTGGCAGGGTCTC
GGCTCACTGCAGCCCCGTCTCAGGTTCAAGCGATTCTCTGCCTCAGCCTCCCGAGTC
[G,A]

CTGGGACTACAGGCGCATGCCACCAGCCCAGCTAATTTTTGTATTTTAGTAAAGACGG
GGTTTTACCATGTTGGCCAGGATGGTCTTGATCTCTTGACTTCATGATCCACCCGCTTG
GCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCACCCCTGGCCAATGTTTGGTATT
TATCTTTAGGTGCTCTGATGTTGGGTTTCATATATATTTATAAAAAACAATAGCTACATAA
CTTATTAAGGGATATGCAATATAAAATATATAAATTGTGACACTGAAAATTTAAATGGG

(SEQ ID NO:85)

24983

TCTGATGTTTCTTACTGATTTTCTGTTGAGATGATTTGTCTATTGCTGAAGGTAGGGTGT
TGAAGTCCCCTACTATTGCTGTATTGCAGTCTCTCTCCTTTGAGACGTATTAATGGTT
TTTATTTTATTTTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTTGGAGACGGAGTCTC
ACTCTGTACCAGGCTGGAGTGCAGTGGCAGGGTCTCGGCTCACTGCAGCCCCGTCTCA
CGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGTCGCTGGGACTACAGGCGCATGCCA
[T,C]

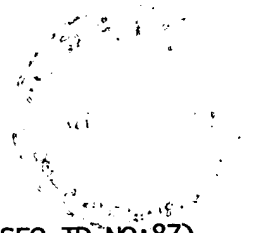
CACGCCCAGCTAATTTTTGTATTTTGTAGTAAAGACGGGGTTTACCATGTTGGCCAGGAT
GGTCTTGATCTCTTGACTTCATGATCCACCCGCTTGGCCTCCCAAAGTGCTGGGATTAC
AGGTGTGAGCCACCACCCCTGGCCAATGTTTGGTATTTATCTTTAGGTGCTCTGATGTTG
GGTTCATATATATTTATAAAAAACAATAGCTACATAACTTATTAAGGGATATGCAATATA
AAATATATAAATTGTGACACTGAAAATTTAAATGGGAGGAGTGAGTAAAAGTACCTTC

(SEQ ID NO:86)

25390

AGTGCTGGGATTACAGGTGTGAGCCACCACCCCTGGCCAATGTTTGGTATTTATCTTTAG
GTGCTCTGATGTTGGGTTTCATATATATTTATAAAAAACAATAGCTACATAACTTATTAAG
GGATATGCAATATAAAATATATAAATTGTGACACTGAAAATTTAAATGGGAGGAGTGGA
GTAAGTACCTTCATATAACTTACTATTATATCCTCTTATTGAATTGACCCTTTTATCA
TTATATAGGAACTTGTCTCTCTTACAACCTCTGACTTAAAGTTTGTCTTATATGATA
[T,C]

FIGURE 3-37



AAGTAAAGTTACTCCTGCTCTCCTTTGGTTTCTGTTTCCATGGAATATCTTTTTCCATTC
CTTCACCATCAGTCTGTGTGATTTTTTACAGATGAAATGAGTCTGTATGGGCAGCATAT
AGTTGGATCTAGTTTTTTTAAATCCACTCAGACACTGTGTTTTTGGATTGGATAATTTAAT
CCATTCATGTTCAAGGTAATTATTGATAAGTAAGGACTTTGTACTACCATTTTGCTTATT
GTTTCATGGTCTTTTATAGATCCTTTATTCTTTCTCCTCTCTTGCTGTCTTTTTTTT

(SEQ ID NO:87)

26060 GGTTTTTGGTTTGTGGTTACCAAGAGGTTACAAAAACATCTTAAGAGTTATAATAGTTT
ATTTTAACTTGATAACTTAATTTTTATTGCAAAAACCCCCAAAAACAAAAAATCTACAC
TTTTACTTAATCCCCTGAAATTTTGAATTTTGTATGTCACAGTTTACCTCTTTTCATATT
GTGTATCCCTTAAATTATTGTAGCTATTATTACTTTTAAATAGTTTCTCTTCTCTACTAC
AGATGTAAGTGATTGTCATACCATCATTACAGTATTATTTGAATTTACCTGTGTACTTT
[C,T]
TTTTATCAGCCAGTTTATACTTTTCTAGATGTTTTTGTGTACTCATTAGCATCTTTTTCT
TTCAGCTTGAGGAGCTCCTTTTACGTTTCTTATAAAATAGGTGCGGTCTAGTATTATCTCC
CTCAGCTATTGTTTGTCTGGGAAAGTATCTCTCCTTCATTTCTGAAGGACACTTTGCTGG
GTACATTACCTTGGTTGGTATTTTCTCCTTGAACGCTTAAATATATCATCCCTTTCT
CTCCTGACCTGTTAGGTCTCTGCTGACCACTGTTTCCAACCATATTGGGACTGTCTTA

(SEQ ID NO:88)

30245 ATTTTAACCATCCATTGTTTCTGCTTCTCTAGATAACCCTGACTAATATATAATTGGTAT
GAAGTGATATCTCATGGCTTTGATTTATATTTCTTTCATGGCTAGTGACTTTTTTGTAC
TTTTGGGATATTGTTATTATTATTATTATTACTAGTGTATACTTCTTCAGTAAAA
GTGTTAGAAACAATTTTAAAGGCAGAATGTGACCAGAGTTTCTGTAGTTATATAACCA
TCATGGACCTTCCCTCAAGTGCTAAGCCATTAGTGTACTCATGTCACTCAAATGTCAG
[C,G]
TTGTTTTCTTCCATTTCACTGTCTCTTGTGTCCAACTTGAATTCATGGGAAAAACAT
CTGAATGGTGCTTAATATGGTTTGGATATTTGTCCCTCCAAATCTCATGTTGAAATATG
ACCTCCAGTGTTGGAAGTAGGGACTACTTGGGTACGAGAGTGATCCTTCATTAATGGC
TTGGTAATAAGTGAACCTATTAGTTTCATGAAAGCTGGTTGTTGATAAGAGCCTGGCATC
TCATTTCTCTTGTCTTCTCTCACCATCTGACACACTTGCTCACCTTTTTTCTTCAGCCA

(SEQ ID NO:89)

33664 TTCCAGAGTGTAGAAGTACACTGTCCTATCCTTTCTAGGAGATCATTATAACACCAAAAG
CAGACAGTATATGAAACAGGGAAATTAGAGGCCAAGATACCTATGACTTATATGTAAAAA
TTTAAAGAAAATATTAGCAAATGAATCAGCCATTTTAAAAAATATACCACAATCAATGC
ATTCATAAGAGCAGCTTAACAAAATTTGTTAGAAGGCATTAAAGAAGACTCAGTATAGAA
AAGATGTACCTTCTCTCAAATTTGGTGATAGAGATTCAATGCCATTAAAAAAACCCACCT
[G,T]
GTTTTTTTGGAGAACTTGTCAAGCTGAGTCTCAAATTTATATCAAAGAGCAAAGGCCTAA
GAATATCCAGGACATTCTGAAGAACTGTAAGGAGCCAGGGCCTGCCCTATCAGATACC
AAGGTTGTTATTAAGCCATAACCAAGTCAGTGCTGTTTCTACAGAAACAGACAAGTTAA
CAAGTGAAACATAATAGAGAGCCAGAAACAGACCCATCCATATTTTGGATTTGTACAGT
GAAAGAAGTAGCTTTGCAAACTTTGGGAAAAGGAGAGTGTGTGCAATAGATGATGCTCG

(SEQ ID NO:90)

33883 TAAAGAAGACTCAGTATAGAAAAGATGTACCTTCTCTCAAATTTGGTGATAGAGATTCAA
TGCCATTAAAAAAACCCACCTGGTTTTTTTGGAGAACTTGTCAAGCTGAGTCTCAAATTT
ATATCAAAGAGCAAAGGCCTAAGAATATCCAGGACATTCTGAAGAACTGTAAGGAGCCA
GGGGCCTGCCCTATCAGATACCAAGGGTTGTTATTAAGCCATAACCAAGTCAGTGCTGTT
TCTACAGAAACAGACAAGTTAACAAGTGAAACATAATAGAGAGCCAGAAACAGACCCAT
[C,A]
CATATTTTGGATTTGTACGTGAAAGAAGTAGCTTTGCAAACTTTGGGAAAAGGAGAGT
GTGTGCAATAGATGATGCTCGTCTCATGCAGACAAAAAGGAAATTTGGATACCTGCCTC
TTACCGTACACAAACACCAACCTAAACGTGAAAGTTAACTATAACAGCTTGAGGTGGTG
GGGAAGAAATATCTTTATCTCAGTGTAAGGAAGAATTTATTTTAAAAAGAAGACACAAAA
GGCCATACATAGGAATGAAAAGATTGAATTGAGCTGCATTAAAAAGATTAAATTCAGCTG

(SEQ ID NO:91)

34373 TATCTTTATCTCAGTGTAAGGAAGAATTTATTTTAAAAAGAAGACACAAAAGGCCATACA
TAGGAATGAAAAGATTGAATTCAGCTGCATTAAAAAGATTAAATTCAGCTGCGTTAAAT
CAAGAGCATCTGTACTTGGACAGCATAGAGTGAAAGACAAAGAGAAGGTATTTGCCAGC
TTATAACTTGAAGGATTAGAATGAATGATATAAAGAAGTATGTAAATAAGAAAAAGACAT

FIGURE 3-38

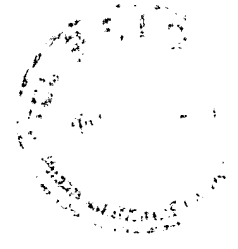
- ACAACCGGTTAGAAAAACGGGCAAAGACATGAACAGCATATTTACGTGAAGGAAACAGC
[G,A]
GTAGCAAATGAACATGGTAAGAGATGCTCAACACGTTTAGTAATTTGAAGGGAAATGCAA
GTTATACCCACAGCAAGACTATCTTATCTAGGAAGTTTGTCAATACCCTAAATGTTCTGT
GGTTTTAAGCTACAGAGTTTGTAAATCATTTATTTATTCAATAAAATACTCAGTGGCAGGC
ACTGTTTTAGAAACCTTGGTTATAACTTTGAATGAAATTAATAAAAAATCCTTGCCTTGTG
GAGGATGCTTATGTGTGGGAGTTGGGTGGTGGGGTCAAACAACAATTACATTAAAAATAG
(SEQ ID NO:92)
- 34558 ACTTGAAGGATTAGAATGAATGATATAAAGAACTATGTAAATAAGAAAAAGACATACAAC
CGGTTAGAAAAACGGGCAAAGACATGAACAGCATATTTACGTGAAGGAAACAGCGGTAG
CAAATGAACATGGTAAGAGATGCTCAACACGTTTAGTAATTTGAAGGGAAATGCAAGTTA
TACCCACAGCAAGACTATCTTATCTAGGAAGTTTGTCAATACCCTAAATGTTCTGTGGTT
TTAAGCTACAGAGTTTGTAAATCATTTATTTATTCAATAAAATACTCAGTGGCAGGCACTG
[G,T]
TTTAGAAACCTTGGTTATAACTTTGAATGAAATTAATAAAAAATCCTTGCCTTGTGGAGGA
TGCTTATGTGTGGGAGTTGGGTGGTGGGGTCAAACAACAATTACATTAAAAATAGAAAAAT
AGTGACATAAATAAACCTATAAATATTGCAACCCAGAGTTATATTATAAATGTAAGTAGT
GACTAGGACTCTCATGCAGATACCTCTGTGCTGGGACAAATGAAAGTTTAAGTGTAAAT
TTCCCATATGCAAGTCAAATAAAAAAGTGACACTAGAAAAACACAATAATGAATATCTGAA
(SEQ ID NO:93)
- 43929 GGCATTTAAGTATTCTGCCATAGGGAAGTGTAAGTTGTAGGCTTTTACTTTTTATAGG
TACTATATTGTCAAATAATCTCAGCACCTCATGGTTGCTAAGGATCTGTGCTTGTGTT
GGTCAGATTATGTTTATCTCTGGCATAAGGCACCTAACAAATATTCATTAAAGGTTACAGA
ATCTTTTTGCTTCATCTGCTTAGCATTTATACCAGTTTGTGTTCCACCAAACCTTCAAA
TTTTGATTGTTTCATTAATATTCTGCATACTGATGTAAACCAAGTTCTATTATTGTGCAA
[T,A]
CTGCTCCTGAAACCTTAGGAACTCTCTGAAGGAGTTTTATTTATTTTTGTTTTGTTT
TTGTTTTGTTTTGTTTTTTTGGAGACGGAGTCTTGCTCTGTTGCCAGGCTAGAGTGCA
TGGTGCGATCTCGGCTCTCTGCAAACTCGGCCTCCGGGTTACGCCATTCTCCTGCCTC
AGCCACCGGAGTAGCTGGGACTACAGGCACCCACCACTGCGCCTGGCTAATTTTTTTTGT
ATTTTTAGTAGAGACGGGTTTCACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTT
(SEQ ID NO:94)
- 44309 TTGAGACGGAGTCTTGCTCTGTTGCCAGGCTAGAGTGCAAGTGGTGCGATCTCGGCTCTC
TGCAAACTCGGCCTCCGGGTTTACGCCATTCTCCTGCCTCAGCCACCGGAGTAGCTGGG
ACTACAGGCACCCACCACTGCGCCTGGCTAATTTTTTTTGTATTTTAGTAGAGACGGGG
TTTACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTTGTAAATCCGCCCGCCTCGCC
TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGTGCCCGGCCTTTTTTTTTTTTTTTT
[T,-,C]
TTTATGGGCTTGTCTTCTACACTTCAGATTTGACTAAATTAATATGCATTAAATGAAGT
CAGGAGTTACATTGCCACTAGTAACAATGCCTAAGCTTACATAAAGCATTATAAAATTG
TTGGTGATTAGTGCTTCTCAGCTATGAGTATAAGATAAATATTATACTAGTAGTTAGTT
GCCTAGATAAATGTACACTATGTGAAGTTTATTTACATAAATCTTACGGTATTTTTTA
AGGTAGTTGATAACAGTTGAGACTACAATTGTATCTCCATTTTATTGATAGTAAAAATGAA
(SEQ ID NO:95)
- 44997 GAATTGTAAAAATATTATTATAGAATTGTTCTCTCAAACCTATAGTAATGTAGAATAGGT
TGAAGGGGTGATGATTTGAAACAATACCTCTCCATTAGCTAAATTTTATATAGAATCTAT
TGCATGTTTTAAATGATAAGTCAGATTTATAAAAAATTTTTATAAACAGTAGGAAATGA
GTTTAGGGGATTACATACAGTTTTAATTTTTTATTACATATTTAAACATATCATGGT
ATAAATATGATGTGGATATAAATTTGAGATAAAGGAAGTATTGTTTAAGAATTGATGAAC
[T,G]
AATTTCTTAAAGATGTCATCACCAGTTGGTTTTCTAGCCTTATGAAAAATGGTTGCAAT
AAAAAGATTGACTATGATAAAATGTGCCCTTTCATTTTAACTAGACCAAGAGAAAAAC
ATACTGTGAATCTATGATGAATGAAAGAAAGTTGTAAGTGTGGTTTTGTATATTTGTAA
TTACTGTTTATTTTCATTTCTTGTGAAGTGAAGTGAAGTGTGTTTATTGTTGAGTAGACA
ACTTATAATCTATGACTCAAATTTGGTTTAGTATAAATTTAGGGAATGAAGTTCATATT
(SEQ ID NO:96)
- 46538 TGTATACTTATGGTCAACACTTTTTATATTTGTCTGTAGATTTCTGTACAAAAAGATTTC
TGACACTGTTTTAAGCCAGCATTCCTTCAGAAATGTACCCAAATCTCAAATTTATTTAGG

FIGURE 3-39



- GGCAAAGCTAATGCTTTAAAGAAAAAGGAGA
[A,G]
GGGATTGGTGTGTGTTTTCTTTAGGAACAGTAGTAACCTGACTTTTAGAGAACTTGAAT
AAGCATTTATTTTTCTTTGTCTATTTTATTGTGAAGTTATTTATTTAAAAATAAAT
GGATTTCTCTGGAATTTAGTTTCTGCAAATTTGAGGAGTTTCAAAGTCAACCTTCAGGT
TTGATACTTCTCTAGAAAGACTCACATAACTCACTGAAAGCTTATTACCCCTGGTTATGG
TTTATTACGGGGAAAAGATGCGGATGAAAATCAGTCAAGTAAAGAAGCACATAGGGCAGA (SEQ ID NO:97)
- 48153 TTATATCATTCTGCTTTTATTTTTAGGTTACGGTTCAAATCAGACAAATGAACATAT
TTGGTGGCTTTTGACAGATGGTAAAAGAAGGAGGTATCCGCTCGCTTTGGAGGGGAAATG
GTACAAACGTCACTCAAATTGCTCCTGAGACAGCTGTTAAATCTGGGCATATGAACAGG
TAATTGTTATCACCCGTGGAATTTATTAACAAAGAGGAGTTAGTAAACGGATTCAATAAA
TGTTAATGTATAATGCTTTTGGGATTCTTGTTTTAATACATGATAATCTTTCACATATAC
[T,C]
CCATAAGGAGGATCACTTATAGGAGATTAGACTAAATAAAATCAGAGATTTCTCATGACC
AAGTTATGGGATTCTTAATTCATCATATTATTTATAAAGTTTTTTTTCTAAGTAGTTT
TTAAAGGAAGGGTAGAATTTTAGTTTATTCTGAATCCTGAGCAGAAGCAGCACACT
AACATAAGTTTTATGAAAGTGTCAATCTAACCTCTGGAAGGAAAACTATAAGTTGAAG
TCCTTTGTGTAATTTGACGTTGCTGTAAAATTGAGCTGAGTTTGGAGTGACACCTCCATG (SEQ ID NO:98)
- 48288 AAATTGCTCCTGAGACAGCTGTTAAATCTGGGCATATGAACAGGTAATTGTTATCACCC
GTGGAATTTATTAACAAAGAGGAGTTAGTAAACGGATTCAATAAATGTTAATGTATAATG
CTTTTGGGATTCTTGTTTTAATACATGATAATCTTTCACATATACCCATAAGGAGGATC
ACTTATAGGAGATTAGACTAAATAAAATCAGAGATTTCTCATGACCAAGTTATGGGATTCT
TTAATTCATCATATTATTTATAAAGTTTTTTTTCTAAGTAGTTCTTAAAGGAAGGGTA
[G,T]
AATTTTAGTTTATTCTGAATCCTGAGCAGAAGCAGCACACTAACATAAGTTTTATG
AAAGTGTCAATCTAACCTCTGGAAGGAAAACTATAAGTTGAAGTCTTTGTGTAATTT
GACGTTGCTGTAAAATTGAGCTGAGTTTGGAGTGACACCTCCATGAAGGCAGGGCGTGG
CTTCTTCCCATGTACTCCAGCACCTAGACAGAGCTTGGCATGTGATAAGTTTCAAGCGA
GTGTTGAATGAGTCAATGAATGAACAAATGCATTTACCTCTGAATCACTTCTCTGTCGGC (SEQ ID NO:99)
- 48412 TGGGATTCTTGTTTTAATACATGATAATCTTTCACATATACCCATAAGGAGGATCACTT
ATAGGAGATTAGACTAAATAAAATCAGAGATTTCTCATGACCAAGTTATGGGATTCTTAA
TTCATCATATTATTTATAAAGTTTTTTTTCTAAGTAGTTCTTAAAGGAAGGGTAGAAT
TTTAGTTTATTCTGAATCCTGAGCAGAAGCAGCACACTAACATAAGTTTATGAAA
GTGTCACAACTAACCTCTGGAAGGAAAACTATAAGTTGAAGTCTTTGTGTAATTTGAC
[G,A]
TTGCTGTAAAATTGAGCTGAGTTTGGAGTGACACCTCCATGAAGGCAGGGCGTGGCTTC
TTCCCATGTACTCCAGCACCTAGACAGAGCTTGGCATGTGATAAGTTTCAAGCGAGTGT
TGAATGAGTCAATGAATGAACAAATGCATTTACCTCTGAATCACTTCTCTGTCGGCTTT
GTTAACTTGGATTATTTGAGCTATTGCTTCAGCCTAACTCAATGTAAAGGGGAAATACAG
AGGTAAGTTTATAGAGTTTGGGTTCTCTTTATGGTCATTAGCAGAAGTGTCTAGTTGAGCA (SEQ ID NO:100)
- 48446 CATATACCCATAAGGAGGATCACTTATAGGAGATTAGACTAAATAAAATCAGAGATTTCT
TCATGACCAAGTTATGGGATTCTTAATTCATCATATTATTTATAAAGTTTTTTTTCTA
AGTAGTTCTTAAAGGAAGGGTAGAATTTTAGTTTATTCTGAATCCTGAGCAGAAGC
AGCACACTAACATAAGTTTATGAAAGTGTCAATCTAACCTCTGGAAGGAAAACTATA
AGTTGAAGTCTTTGTGTAATTTGACGTTGCTGTAAAATTGAGCTGAGTTTGGAGTGACA
[C,G]
CTCCATGAAGGCAGGGCGTGGCTTCTTCCCATGTACTCCAGCACCTAGACAGAGCTTG
GCATGTGATAAGTTTCAAGCGAGTGTGTAATGAGTCAATGAATGAACAAATGCATTTACC
TCTGAATCACTTCTCTGTCGGCTTTTGTTAACTTGGATTATTTGAGCTATTGCTTCAGCC
TAACTCAATGTAAAGGGGAAATACAGAGGTAAGTTTATAGAGTTTGGGTTCTCTTTATGGT
CATTAGCAGAAGTGTCTAGTTGAGCAGCCACAGATTATGTTTTCCATTATTTATTCATC (SEQ ID NO:101)
- 48456 ATAAGGAGGATCACTTATAGGAGATTAGACTAAATAAAATCAGAGATTTCTCATGACCAA
GTTATGGGATTCTTAATTCATCATATTATTTATAAAGTTTTTTTTCTAAGTAGTTCTT

FIGURE 3-40



AAAGGAAGGGTAGAATTTTAGTTTATTTCATTCTGAATCCTGAGCAGAAGCAGCACACTAA
CATAAGTTTTATGAAAGTGTCACAATCTAACCTCTGGAAGGAAAACTATAAGTTGAAGTC
CTTTGTGTAATTTGACGTTGCTGTAAAATTGAGCTGAGTTTGGAGTGACACCTCCATGAA
[G,C]
GCAGGGCGGTGGCTTCTTCCCCATGTACTCCAGCACCTAGACAGAGCTTGGCATGTGATA
AGTTTCAAGCGAGTGTGAATGAGTCAATGAATGAACAAATGCATTTACCTCTGAATCAC
TTCTCTGTGCGGCTTTTGTAACTTGGATTATTTGAGCTATTGCTTCAGCCTAACTCAATG
TAAAGGGGAAATACAGAGGTAAGTTTATAGATTGGGTTCTCTTTATGGTCATTAGCAGA
ACTGTCTAGTTGAGCAGCCACAGATTATGTTTCCATTATTTATCCATCATTGTTTATC

(SEQ ID NO:102)

48789 GCACCTAGACAGAGCTTGGCATGTGATAAGTTTCAAGCGAGTGTGAATGAGTCAATGAA
TGAACAAATGCATTTACCTCTGAATCACTTCTCTGTGCGGCTTTTGTAACTTGGATTATT
TGAGCTATTGCTTCAGCCTAACTCAATGTAAAGGGGAAATACAGAGGTAAGTTTATAGAGT
TTGGGTTCTCTTTATGGTCATTAGCAGAACTGTCTAGTTGAGCAGCCACAGATTATGTTT
TCCATTATTTATCCATCATTGTTTATCAAGGACTGTAAAGGCCTTGAATTCACCTCCC
[C,-]
CCCCCATAGTTTTTGTATTATTCATGTAGATTTTAGATTATTTCTGGAGAGTGTTTTGT
CTTGAGCAACAGAACTACTCTTGAGAAGATTACGAAGTCCAGTGGTATCCTTTTCTTTGCC
TAGGAAATAGAGAAGCAAAAAAAAAAAAAAAAAAAATTAAGAAAATCTAGTCTCCAGG
ATTTTAATTAGAACCTATCCTTGGGAAGGCTATTTTCCCTATATGAAGGTTTGAAGATTC
AATCATGATTATTAAGGGCTAATGTTTGAGATACCCTTAGGTTATTCTGACCACATACT

(SEQ ID NO:103)

48859 CATTTACCTCTGAATCACTTCTCTGTGCGGCTTTTGTAACTTGGATTATTTGAGCTATTG
CTTCAGCCTAACTCAATGTAAAGGGGAAATACAGAGGTAAGTTTATAGAGTTGGGTTCTC
TTTATGGTCATTAGCAGAACTGTCTAGTTGAGCAGCCACAGATTATGTTTCCATTATTT
ATCCATCATTGTTTATCAAGGACTGTAAAGGCCTTGAATTCACCTCCCCCCCCCATAG
TTTTTGATTATTCATGTAGATTTTAGATTATTCTGGAGAGTGTTTGTTCTTGAGCAA
[G,C]
AGAATACTCTTGAGAAGATTACGAAGTCCAGTGGTATCCTTTTCTTGCCTAGGAAATAG
AGAAGCAAAAAAAAAAAAAAAAAAAATTAAGAAAATCTAGTCTCCAGGATTTTAATTA
GAACCTATCCTTGGGAAGGCTATTTTCCCTATATGAAGGTTTGAAGATTCAAATCATGAT
TATTAAGGGCTAATGTTTGAGATACCCTTAGGTTATTCTGACCACATACTTGGATTTTAT
GATAGGAAAGCCACAGCCTAAAATAAATAAATACTCAATGCAGTTATTTAGTATGCAAG

(SEQ ID NO:104)

49126 GATTATTCTGGAGAGTGTTTTGTCTTGAGCAACAGAATACTCTTGAGAAGATTACGAAG
TCCAGTGGTATCCTTTTCTTTGCTAGGAAATAGAGAAGCAAAAAAAAAAAAAAAAAAAAA
ATTAAGAAAATCTAGTCTCCAGGATTTTAATTAGAACCTATCCTTGGGAAGGCTATTTT
CCTTATATGAAGGTTTGAAGATTCAAATCATGATTATTAAGGGCTAATGTTTGAGATACC
CTTAGGTTATTCTGACCACATACTTGGATTTTATGATAGGAAAGCCACAGCCTAAAATAA
[A,G]
TAAATACTCAATGCAGTTATTTAGTATGCAAGAAGTTTGGTATTTTGAAGAAAGTCCAT
GGGTATTGCAAGCAAATATGCACATTTTGTCTTTATGCCATTTGTGAGATTCTTACCTTGG
ATACCACCAACAGGCATCCTCTGCTTCTGTCCACCAAGCTCCTTCTGAGACCTCTTTA
TAGTATTGTGATTTCTGCACACTAACTTTCTTAGACATGAAGAGAAAGCTGTCTACACAG
TGTGGTGTAGTTTCTTATGGGCTCTGGACCTATGGTGCTGTTTCTCTCCTCCTGCTGA

(SEQ ID NO:105)

49378 TGACCACATACTTGGATTTTATGATAGGAAAGCCACAGCCTAAAATAAATAAATACTCAA
TGCAGTTATTTAGTATGCAAGAAGTTTGGTATTTTGAAGAAAGTCCATGGGTATTGCAA
GCAATATGCATTTTGTCTTTATGCCATTTGTGAGATTCTTACCTTGGATACCACCAAC
AGGCATCCTCTGCTTCTGTCCACCAAGCTCCTTCTGAGACCTCTTTATAGTATTGTGA
TTTCTGCACACTAACTTTCTTAGACATGAAGAGAAAGCTGTCTACACAGTGTGGTGTAGT
[T,G]
TTCTTATGGGCTCTGGACCTATGGTGCTGTTTCTCTCCTCCTGCTGAAGGTCCATTCAT
CCCTCGGGGCTCTCTAAAGCCACCTTCTGTGACAAGCATATACTAAGCATCTCAATCA
AAGCCAGTTCTCCCCTGTCCAGCCTCCCTCGAGTGCTGAATTGCAGAATATCCCATT
TCATTGGATGATGGAACCCATTGTTTCCAGTGGATTGTAAATTAATTCGGGGTAAA
TAGGCTGTATATATTCTCAAATTTCCAGAGTATGTAAGTGGTCACTTTTAGATTCAGA

(SEQ ID NO:106)

FIGURE 3-41



- 49482 TCCATGGGTATTGCAAGCAAATATGCACATTTTGCTTTATGCCATTTGTGAGATTCTTAC
CTTGATACCAACAGGCATCCTCTGCTTCTGTCCACCAAGCTCCTTCCTGAGACCT
CTTTATAGTATTGTGATTTCTGCACACTAATTTCTTAGACATGAAGAGAAAGCTGTCTA
CACAGTGTGGTGTAGTTTTCTATGGGCTCTGGACCTATGGTGCTGTTTTCTCTCCTCT
GCTGAAGGTCCATTCATCCCTCGGGGCTCTCTAAAAGCCACCTTCCTGTGACAAGCATAT
[A,C]
CTAAGCATCTCAATCAAAGCCAGTTCTCCCCTGTCCAGCCTCCCTCGAGTGCTGAATTG
CAGAAATATCCCATTTTTTCATTGGATGATGGAACCCATTGTTTTCCAGTGGATTGTAA
ATTACTTCGGGGTAAATAGGCTGTATATATTCTCAAATTTCCAGAGTATGTAAGT
CACTTTTAGATTGAGATAGATTTTGTTCCTGAATAGCTAGTACTTTAGGAACTAAGAA
AAAGATCTTTTCAACCTGGTATGTAGCTCTGTCAAACACATCATCAGTATGGGGTAAACC (SEQ ID NO:107)
- 49741 CTCGGGGCTCTCTAAAAGCCACCTTCCTGTGACAAGCATATACTAAGCATCTCAATCAA
GCCAGTTCTCCCCTGTCCAGCCTCCCTCGAGTGCTGAATTGCAGAATATCCCATTTTTTC
ATTGGATGATGGAACCCATTGTTTTCCAGTGGATTGTAAATTACTTCGGGGTAAATA
GGCTGTATATATTCTCAAATTTCCAGAGTATGTAAGTGGTCACTTTTAGATTGAGATA
GATTTTGTTCCTTGAATAGCTAGTACTTTAGGAACTAAGAAAAAGATCTTTTCAACCTG
[G,A]
TATGTAGCTCTGTCAAACACATCATCAGTATGGGGTAAACCTGTGTTCTCTGTGGGTTGT
CATTACCATAGTAGTGTCATTGTATCATTGACAGTGTAATAGTGTGGGGTAGTGTTCTTG
TGGTTTCAGCTGCCACTCTGTACTGACTGCTTCCACTCCA (SEQ ID NO:108)
- 49840 ATCTTTTCAACCTGGTATGTAGCTCTGTCAAACACATCATCAGTATGGGGTAAACCTGTG
TTCTCTGTGGGTTGTCATTACCATAGTAGTGTCATTGTATCATTGACAGTGTA
[A,G]
TAGTGTGGGGTAGTGTTCTTGTGGTTTCAGCTGCCACTCTGTACTGACTGCTTCCACTC
CAACATCTTCTCTTTATCTCAACACTGTAGGTCTACCTGTGTACTGTGTGTTTCAGCAT
CTCTGCTTGCATGACCCAGGAGTGCTCCCACTCAATATGGCCACCATGCATGGTCATCT
TTCTGCTACTCCCTGTCTCCTGACCCTGCTCCAGCAACACAGACAGACACCCTTCTCTT
TCTATATGTCATATGGTGGGAATGCCCTTTAGTACTTACTCAGGAGTTAGTTCTCTGG (SEQ ID NO:109)
- 50102 CATTACCATAGTAGTGTCATTGTATCATTGACAGTGTAATAGTGTGGGGTAGTGTTCTTG
TGGTTTCAGCTGCCACTCTGTACTGACTGCTTCCACTCCAACATCTTCTCTTTATCTC
AACACTGTAGGTCTACCTGTGTACTGTGTGTTTCAGCATCTCTGCTTGCATGACCCAGGA
GTGCTCCCACTCAATATGGCCACCATGCATGGTCATCTTCTGCTACTCCCTGTCTCCT
GACCCTGCTCCAGCAACACAGACAGACACCCTTCTCTTCTATATGTCATATGGTGGGG
[G,A]
ATGCCCTTTAGTACTTACTCAGGAGTTAGTTCTCTGGGAAGCCTTCTGTTCTAGTTTCC
TTTTGTTACAGCACTTTCACATTGAATTCTGACGTTCTCTGTACTTATCTGCTTTGTGAG
ACTGTGAGCTTCTTAGGCAGTAGCTACTTGTATTCTTAGCACCTTGCCAGTGCCAGGA
AACCTTATTAAAGTAAATGAAAAGACAGAACTGACAGACTGGAATTAGAGCTCAAGCTTG
CCTCAATCTCAAGCCATTAAGATGAAGGGGAGCCGGGCGTGGTGGCTCACGCCTTAATC (SEQ ID NO:110)
- 50109 ATAGTAGTGTATTGTATCATTGACAGTGTAATAGTGTGGGGTAGTGTTCTTGTGGTTTC
AGCTGCCACTCTGTACTGACTGCTTCCACTCCAACATCTTCTCTTTATCTCAACACTG
TAGGTCTACCTGTGTACTGTGTGTTTCAGCATCTCTGCTTGCATGACCCAGGAGTGCTC
CCTCAATATGGCCACCATGCATGGTCATCTTCTGCTACTCCCTGTCTCCTGACCCTG
CTCCAGCAACACAGACAGACACCCTTCTCTTCTATATGTCATATGGTGGGAATGCC
[C,G,T]
TTAGTACTTACTCAGGAGTTAGTTCTCTGGGAAGCCTTCTGTTCTAGTTTCTTTTGT
ACAGCACTTTCACATTGAATTCTGACGTTCTCTGTACTTATCTGCTTTGTGAGACTGTGA
GCTTCTTAGGCAGTAGCTACTTGTATTCTTAGCACCTTGCCAGTGCCAGGAAACCTT
ATTAAGTAAATGAAAAGACAGAACTGACAGACTGGAATTAGAGCTCAAGCTTGCTCAAT
CTCAAGCCATTAAGATGAAGGGGAGCCGGGCGTGGTGGCTCACGCCTTAATCCAGCAC (SEQ ID NO:111)
- 50747 CCAGCCTGGGCAACGTGGCAAAACCCCATTTCTACAAAAAATATAAAATTAGTTGGACG
TGGGGGTGTGTGCCTGTACTCAGGATGCTGAGGTGGGAGGATCACTTGAGCTCGAGAGGC
AGAGTTGCAGTGAGCTGGGATCACACCATTGCAATCTAGCCTGGGTGATAGAATGAGAC

FIGURE 3-42



CTTGTCTCAAAAAAAAAAATAAATAAATAAATAAAGGGGAAGATAAGGATTGGAAACAGAA
GGAGCAGCATGTGGACAGAAATGTAGGCACAAGAAGGCATCACTCACTGAAGAGACTGAA
[G,A]
GTGGTTCACTGTGCCTCAAGACTGGTGGAGTGTGTTTCCGGAAGATAATGATGAAAGAG
CTGGACAGATAAACAGGGGCCAAATGTAATAGGAGTCTGGATTTTATTCTGAATATGGTA
GGGGCTATTGTAGCATCTTATATAGGGAAGTGAATGAGTACATTACATTTAAGGAATA
TCAACCTGAAAAAAGAGTGGAGACATTGTTGGGGGAGAGTGAGGTAGACTAGAGGCAGGG
AGAATATTTAAATAATTGAGGTAAGAAATGATGAACACCAGTATAAGGTGATGTCTTTAA

(SEQ ID NO:112)

51272 TAGACTAGAGGCAGGGAGAATATTTAAATAATTGAGGTAAGAAATGATGAACACCAGTAT
AAGGTGATGTCTTTAAGGAATGGAGAAGGGAATGAACTGAGAAATATTTTGGAAGTAGAA
TCAACAGAACTCACTGACTGACTGGATATGGAGGTGAGAAAGAGAAGAGTCAAGAATGAT
ATTCTAATTTCTAACTTGAGTGAATGCAATCAAAGAGAATACAATATCAGGTTCCATTTT
GTGCTGCTGAGTTTGAGATGTGTGGGACATGTACAGGGAGCTGTCCAGTAAGCAATTGG
[G,A]
TATATCAGCTAGCCATTAAGAGAGAGATCTTTGATAGAGAGGTTGTTGCTGAGTTGAGCC
ATTGGAATGGGCAGGATCACTCAAGAAGAGCTTATAAATGAGAAGAATTCTAGGAATAAG
TCCAAAGGGAGAAGTAAAAGAAGAACTTGCAAAGGACACTGAGAAGAAATAGCTCGAGG
GATGGGAGAAAATCCAGAGAGAGGGATGGCATAGGAGTCAGTGGAAGGAAACGGTTTCAT
GGGGGTCAGTACTACTGGGTAGTGAATATAATAAGAAATATCTTTTAGGATTTCTCAACCC

(SEQ ID NO:113)

52842 TCAGGGTGGTTTTGAGGGCTCAGTTAAGTCTCTTTAGGAAGGTTCAAGTCTGTAGCCTT
GGCAAGTTACTTAAAGTCTCTGTGACTATTACCTCATCTCTAAGATGGGGACTAAGCTTG
GTGACATAGTTTTACATACCAGGCACAGTGCCTGACTTTTGGCTCTGTCTGAAGTCTT
CCCTTTGTATATGGTATGTTTCGGGGAATAGGAGCCTCAAGCACTTATCCTTTAAATATT
TATCCTCCATCAGTCACTAAACGTTTACTCTGTACTTTTGATAGGTGCTGTGGGGTCCA
[G,A]
GGTATAAAAGGTACCTTCAAAGTTACTGTTAAAGTGCAGGAAGGTTTTTAAGCAAATTAT
GTTTAATGATTTTGACAATCTGACATGCAGGAAAAATTAATAGGGCCTATGCAGAAGAGGA
GTTTTATGTAACACTCTGTAGTTCAAGAAACAGAGCCCTTGAAGCAGTGATCTCTCTGG
GGAGGAATGTCTGGTATTTGGGAATCTCATGAAATGATAATATACTTAATTTTTATCATG
AGCAGCAAAACACAGATTTGCTAGGAGAAAGTCATCGTATGTTGTTGCATTGGGCACCTT

(SEQ ID NO:114)

61837 GAGGAACCTCCATGTCAATTTTCCATAGTAAGTACCTTTTTGTTTTTAAACATTTCTAT
CAATGTACACCAAGATTCCAATTTCTCCATGTCCTCCCCAACACCATTAAGTGGGGTGGT
GGTCTACTACTATTGCTGTGTTGCTGTTTATTCCTCCCTCAGTCTGTAAAGTGTGCT
TCATATATTTAGGAGCTTAATATTAGGTCCATATGAAGTTATAATTTCTCCTGGTAAAG
TGACCCATTTATCATTATGTAATGTCCATCTTTGTCTCTGTGACAGTTGTGTCTTAAA
[A,G]
TCTATTTTGTCTGATGTAATTATGGCCACCCCTTTTCTCTTTGGGTTCCTGTTTTATGG
AATATCTTTTCCATCCTTTCACTTTAGCTTATGTGTGTCCTTAGATCTAAAGTGAGTC
TCATAGATAAGGTATAGTTGATTCTGTATGTGTTATCACTCAGCAATTTATATCTTTTA
GTTAGGGGATTTAATCCATTTACATTTAAAGCAGTTACTGATAGGGAAGGACTTACTGTT
GTCATTTGGCTAGCTACCTTTTTATCTTTGTCTGTGGCTTTTCTGTTTTCCCTTCCTC

(SEQ ID NO:115)

62018 CATATATTTAGGAGCTTAATATTAGGTCCATATGAAGTTATAATTTCTCCTGGTAAAGT
GACCCATTTATCATTATGTAATGTCCATCTTTGTCTCTGTGACAGTTGTGTCTTAAAA
TCTATTTTGTCTGATGTAATTATGGCCACCCCTTTTCTCTTTGGGTTCCTGTTTTATGG
AATATCTTTTCCATCCTTTCACTTTAGCTTATGTGTGTCCTTAGATCTAAAGTGAGTC
TCATAGATAAGGTATAGTTGATTCTGTATGTGTTATCACTCAGCAATTTATATCTTTTA
[A,G]
TTAGGGGATTTAATCCATTTACATTTAAAGCAGTTACTGATAGGGAAGGACTTACTGTTG
TCATTTGGCTAGCTACCTTTTTATCTTTGTCTGTGGCTTTTCTGTTTTCCCTTCCTCT
CTTCCTGGCTTCTCTGTGTTTTGTGATTTTTTTTTTTTGTAGTGATATGTTCTGAT
TCCCTTCTCATTTCCCTTTGTGTGCATTCTATAGATGCTATTTTGTGGTTACCATTGCA
ACTACATAAAGCATACTAAAGTTATAGCAACTATTTTAAAGCTGTTTACAACCTTAACCTC

(SEQ ID

NO:116)

FIGURE 3-43

- 65562 GACTGAAATTCAGACACATGCACTCTGATTCTAACCCTCCTGTCTGCCAGCTCTGATCCA
GAACTTTGCATGACTGATACGGCTGATAGATTGTCTATGGCTGATAGACTGTCAATTTCTG
ACCTAAAAGTCTGATCATTTTACATCTGTTTACAGACATCTTTGCAGCCTTTTCGGTGTGAGT
TCCAAAGTTGTTAGTGGGAATTTCAAAGCCTTTAATAATCTAGCCCCACTTTGTTCACTC
TCTGTGTAATAACCACATACAACAATTGGCTGCATCTCCATAGCACATGGTACTCCTCCC
[A,G]
TTGCTTTGGTTGTGCCAGCAACTGGTTTTGCTTTCTCTTCTGCTTGTGAGGTCAT
TTCCAAGGCCAGGTCTTTGTGCTTTTTCCCAAGCTTCCAGAGCTTCTTCCATACTCCC
CTTACTTCTGAGATTTAACTGTTCTCTCTTTCAGCGCTTGTCTAGTAAGAAGGAGGCAGC
AGCAGCACTGTGGGGTGGTGGAAAGTGTACCAGCTTTGGAGTCAGACCATTGGATCTCAG
CCCTACCATTTTCTACTTAGATTTTTTGGACAAATTTCTCCATCTTTCTAAGCCTCCA (SEQ ID NO:117)
- 65780 TCTAGCCCCACTTTGTTCACTCTCTGTGTAATAACCACATACAACAATTGGCTGCATCTC
CATAGCACATGGTACTCCTCCCGTTGTCTTGGTTGTGCCAGCAACTGGTTTTGCTTTT
CTCTTCTGCTTGTGAGGTCAATTTCCAAGGCCAGGTCTTTGTGCTTTTTCCCAAGCTT
CCCAGAGCTTCTTCCATACTCCCCTTACTTCTGAGATTTAACTGTTCTCTCTTCAGCGC
TTGTCTAGTAAGAAGGAGGCAGCAGCACTGTGGGGTGGTGGAAAGTGTACCAGCTTT
[G,A]
GAGTCAGACCATTGGATCTCAGCCCTACCATTTTCTACTTAGATTTTTTGGACAAATTT
TCTCCATCTTTCTAAGCCTCCAATTGCTCACTTACAAAATTGATATAACATTTACCTTGC
AAGATTGGTATGGAAGGTAATTAACCCAGTATTTAGAACATAGTAATTAATAAAATACTA
TTATTACCATCATTACTATAGTTAGGACACTCACTGTTAGGTGCTATACAAAGAGGATCA
TAAAAGGATGTTGTCTTGGGCTTCTTGAATAAATGTTGCTCTTTACTGTATTTTGA (SEQ ID NO:118)
- 66092 TTGGATCTCAGCCCTACCATTTTCTACTTAGATTTTTTGGACAAATTTCTCCATCTTT
CTAAGCCTCCAATTGCTCACTTACAAAATTGATATAACATTTACCTTGCAAGATTGGTAT
GGAAGGTAATTAACCCAGTATTTAGAACATAGTAATTAATAAAATACTATTATTACCATC
ATTACTATAGTTAGGACACTCACTGTTAGGTGCTATACAAAGAGGATCATAAAAGGATG
TTGTCTTGGGCTTCTTGAATAAATGTTGCTCTTTACTGTATTTTGAATATCATTCTG
[G,A]
GTCATAATTGTTTGTGTGTCATAATAATGAAACATACTTGAATATTAATTAACCTCTTTT
TTTATTTTTTAGCCATGTTAGAAGGTTCCCCACAGCTGAATATGGTTGGCCTCTTTTCGAC
GAATTATTTCAAAGAAGGAATACCAGGACTTTACAGAGGCATCACCCCAAACCTTCATGA
AGGTGCTCCCTGCTGTAGGCATCAGTTATGTGGTTTATGAAAATATGAAGCAAACCTTAG
GAGTAACCCAGAAATGATGTTGCATTTTTTGTCTTAGCCTGATAATTGAAACTTTCAACA (SEQ ID NO:119)
- 66617 ATGAAGCAAACCTTTAGGAGTAACCCAGAAATGATGTTGCATTTTTTGTCTTAGCCTGATA
ATTGAAACTTTCAACAATCTCTGGAGTGACTTTTTCTCCTCGAATTGAAACAAGTCTATG
GCAAAAAGAGCTGCATTTTTTTCACAAAAGGGAAGATGGTAACAATGGTCACTTCAAAC
TTTGGGCTAAATTATATGTACACAGAAATGTTCAAAATCATAGTTTAAATGTGTTTTGAA
AAGGCCACACAATTATACTTTATCTTTCTTAATAATCCTGCAAATCTCTGCCCTGAATC
[C,T]
GAAATCTGAAAATGTACTGGCTTGAACAAAATTTGTTTTGTGTGTTAGAGTTATAAATCA
TTAATCTTTATTTTCGGGTGGTTTACGTTTATGCCAGTTCCTTTATATTTAAATTTCTGT
TTTATATATTTGAATGTCTTTATAGATTTCTTTAAATTTCTTATAGAACCATTAAATAG
AAAATCATTACATTTAAAATATACCTTACAGCAAAAGCATCAAATAAGTATAGGGTTTA
TGCTCTATTTTTCTTTAGCTGAATACGAATGAGCACAGTGGTGAATTTCTGAAGGGA (SEQ ID NO:120)
- 66892 ATCCTGCAAATCTCTGCCCTGAATCCGAAATCTGAAAATGTACTGGCTTGAACAAAATTT
GTTTTGTGTGTTAGAGTTATAAATCATTAATCTTTATTTTCGGGTGGTTTACGTTTATGCC
AGTTCCTTTATATTTAAATTTCTGTTTTATATATTTGAATGTCTTTATAGATTTCTTT
AAATTTCTTATAGAACCATTAAATAGAAAATCATTACATTTAAAATATACCTTACAGCAA
AAGCATCCAATAAGTATAGGGTTTATGTCTTATTTTTCTTTAGCTGAATACGAATGA
[G,A]
CACAGTGGTGAATTTCTGAAGGGAAGTGATGAAATTATATTTATTTTCACTGGGCACTTT
TCCATTTTACCACTGTACCATTATTTGGTTCCTGGAGTTATACACTAATTTTCACTATAT
TACTGTTAAATTACCAACACAAGGCAATTTATTTGAAAGATTCGTTTATCCTGCCATTG
CTTTGAAAAGCAGCAGGAAACGAAATCCTTTGACTTGTATCAGCTTCTGCAGAGCATCTT

FIGURE 3-44

- TGTTTTCTTTTGCTCTTTGTTTCCTACCTTTTGAATCAGATTCCGTTTTAGTCAGGAAGA (SEQ ID NO:121)
- 67263 CACTGTACCATTATTTGGTTCCTGGAGTTATACACTAATTTTCAGTATATTACTGTTAAA
TTACCAACACAAGGCAATTTATTTGAAAGATTCCGTTTATCCTGCCATTGCTTTGAAAAG
CAGCAGGAAACGAAATCCTTTGACTTGTATCAGCTTCTGCAGAGCATCTTTGTTTTCTT
TGTCTTTGTTTCCTACCTTTTGAATCAGATTCCGTTTTAGTCAGGAAGACTTCTTGGGA
CCATTCTTAGTAACCTGAAATTTCTTTTTTAATTGCATGAAGTGGATTGATCATGAGCAA
[G,A]
TGATGTGCTTATTTCTCCCTCACTGTTGAATATCTTTGAACTTGCTGTTTTCAATATGGG
CAGCACAAAGGTGAGAGATACATATTAATAGTAGTATGTATTACTCTTATACATTAGATA
CCTATATTTAAATGAAAGGCCCAATTTGTAAACATATACATTCATATTCTCTCTTGCCCC
AAGTTTTAGGAACATGTTAGGATATAGGAGACTTAATTTATAATAATGAGAGCATTTTTT
TATTTTACTAAAGCCATTTTTATAGTCAACTATCTTTCTTATTTGTGTGATTAGAACTT (SEQ ID NO:122)
- 67651 ATAGTAGTATGTATTACTCTTATACATTAGATACCTATATTTAAATGAAAGGCCCAATTT
GTAAACATATACATTCATATTCTCTCTTGCCCCAAGTTTTAGGAACATGTTAGGATATAG
GAGACTTAATTTATAATAATGAGAGCATTTTTTATTTTACTAAAGCCATTTTTATAGTC
AACTATCTTTCTTATTTGTGTGATTAGAAGCTAGAAAAATATTTACTAGTTGAAGTTAT
TATCAGTTTTTAATTTAGTTCCTTAAACTCATTTCACTCTAATAATTTCTGTTATAAATT
[G,T]
CCAGCATTTTAATGAAAATCTAATGATGTAATAGGCATTTTTCTTATTTGAACCTACCTC
TTTTATTTCTGAACCAAAGAGAAAGATGGACTGGTGTGTTGTGAAACATTTTTAAAAATG
TAGTTTCATTTATATTAGTTATGTTTGATAAATGTCTCAGTATTTTATAATATGATAAG
CCTGGGATTCTACTTTTAGGGTTATTTGACTTTTGAGTAATATATAAAGTGACAATATT
AAGGTACATGATCAGCTCTTTCTATTTTTACTCGTAAAAATATGGAATGAATAATTTT (SEQ ID NO:123)
- 67935 ATTTCTGTTATAAATTGCCAGCATTTTAATGAAAATCTAATGATGTAATAGGCATTTTCT
TTATTTGAACCTACCTCTTTTATTTTCTGAACCAAAGAGAAAGATGGACTGGTGTGTTGTG
AAACATTTTTAAAAATGTAGTTTCATTTATATTAGTTATGTTTGATAAATGTCTCAGTAT
TTTTATAATATGATAAGCCTGGGATTCTACTTTTAGGGTTATTTGACTTTTGAGTAATA
TATAAAGTGACAATATTAAGGTACATGATCAGCTCTTTCTATTTTTACTCGTAAAAATTA
[C,T]
GGAAATGAATAATTTTGCTAACAACTTTGAAATTTCAAACCTTCTGAAAATATGAAAATA
TTCATTGTTTATTATGAATTTAAATTTGAAGGTATGAATGTGATTTGTCTGTACATCTTG
TATCTTTTCCAAAAAATGATTCTGTATCTTTTGAAAAAAGCCGAGAGTTGAAGATAGTA
TATTTCTGGTAGTACTGAATATTTACTTACAGTTTCTATCAAAAATATATATTTGTTTCT
AAAATTAAGTTGTTTTCCAGTTTTTATTTTTTTAGAGAAAATCTTAAGTCTCAGTTTCC (SEQ ID NO:124)
- 69000 TTCAGAAATAACTTATCAGTTATTTCTGTAAGCTTCTTGCTTACCTGGATACCTGACAGG
TGAGATGGCTGTAGCAGACACTGGCAGTTCCCTGCCCACACACCTGTCCCTGTCCACAGC
TGCACAAGGCAGCTCTGTGTGCAATTGCCAGCATCTGCTCCTCTGTTCTCAGGGAATCTT
TGTTAGAAAAATGCTGCCATATTTGTTTCTCACCTATTAGTCTTGTCTCCAGTCAAGAG
AATAAATTTATGCAAGCAGAGATTGTACTTTACAGTATTTTGTCTTTGAGCTTGGCATT
[T,G]
GTTGCATTTGTAAAAATGTGGCATGGCTTCTCATCCCCCAATAGGAACTTTGCCAGCCC
TTTTGTTCTCATGGAACCTCCTTTTTTGAAAAGAGCACCAAAGGAGTAAAAATACTGTGG
AGGGAGCAACCCCTCCTTTGCCATATGCTCTCATTGGGAGACATGTGGAGCAGTCTGAAGT
CATTTAGGCCACTCTCTGGGAGAGCACATCCTATGATGTTCTCCAGCCTAGCCCCCTTCC
ACTGTGCTCAAGTCCAAGCTGACCAGCTTCTGACCACAGTGTAAACAAAGATGATTGTC (SEQ ID NO:125)
- 69134 CTGTGTGCAATTGCCAGCATCTGCTCCTCTGTTCTCAGGGAATCTTTGTTAGAAAAATGC
TGCCATATTTGTTTCTCACCTATTAGTCTTGTCTCCAGTCAAGAGAATAAATTTATGCA
AGCAGAGATTGTACTTTACAGTATTTTGTCTTTGAGCTTGGCATTAGGTTGCATTTGTAA
AAATGTGGCATGGCTTCTCATCCCCCAATAGGAACTTTGCCAGCCCTTTTGTCTCATG
GAACCTCCTTTTTTGAAAAGAGCACCAAAGGAGTAAAAATACTGTGGAGGGAGCAACCCCT
[C,T]
CTTTGCCATATGCTCTCATTGGGAGACATGTGGAGCAGTCTGAAGTCATTTAGGCCACTC
TCTGGGAGAGCACATCCTATGATGTTCTCCAGCCTAGCCCCCTTCCACTGTGCTCAAGTC

FIGURE 3-45

Docket No.: CL001103
Serial No.: 09/777,921
Inventors: Gennady MERKULOV et al.
Title: ISOLATED HUMAN TRANSPORTER ...

CAAGCTGACCAGCTTTCTGACCACAGTGTAACAAAGATGATTGTCAGTGGGCCCCAGAA
TCCTATACCCAGA (SEQ ID NO:126)



FIGURE 3-46

```

1  CCGCAACCCC GACGGCGCCC CAAACGCTGT TGCGCCGCGC GCCCCGCCCA
51  GCCCCGCCTC GCGCTGGTCC CGGTCTCGCC CCGCAGCCCT CGATCTCCCG
101 TGACTTCCTC GGCCAGGCCG CCTGCGCCTC TGGGACCATG TTGCGCTGGC
151 TGCGGGACTT CGCGCTGCCC ACCGCGGCCT GCCAGGACGC GGAGCAGCCG
201 ACGCGTACG AGACCCTCTT CCAGGCACTG GACCGCAATG GGGACGGAGT
251 GGTGGACATC GCGGAGCTGC AGGAGGGGCT CAGGAACCTG GGCATCCCTC
301 TGGGCCAGGA CGCCGAGGAG AAAATTTTFA CTA CTGAGAGA TGTCAACAAA
351 GATGGGAAGC TGGATTTTGA AGAATTTATG AAGTACCTTA AAGACCATGA
401 GAAGAAAATG AAATTGGCAT TTAAGAGTTT AGACAAAAAT AATGATGGAA
451 AAATTGAGGC TTCAGAAATT GTCCAGTCTC TCCAGACACT GGGTCTGACT
501 ATTTCTGAAC AACAAGCAGA GTTGATTCTT CAAAGCATTG ATGTTGATGG
551 GACAATGACA GTGGACTGGA ATGAATGGAG AGACTACTTC TTATTTAATC
601 CTGTTACAGA CATTGAGGAA ATTATCCGTT TCTGGAACA TTCTACAGGA
651 ATTGACATAG GGGATAGCTT AACTATTCCA GATGAATTCA CGGAAGACGA
701 AAAAAATCC GGACAATGGT GGAGGCAGCT TTTGGCAGGA GGCATTGCTG
751 GTGCTGTCTC TCGAACAAGC ACTGCCCTT TGGACCGTCT GAAAATCATG
801 ATGCAGGTTG ACGGTTCAAA ATCAGACAAA ATGAACATAT TTGGTGGCTT
851 TCGACAGATG GTAAAAAGAG GAGGTATCCG CTCGCTTTGG AGGGGAAATG
901 GTACAAACGT CATCAAAATT GCTCCTGAGA CAGCTGTTAA ATTCTGGGCA
951 TATGAACAGT ACAAGAAGTT ACTTACTGAA GAAGGACAAA AAATAGGAAC
1001 ATTTGAGAGA TTTATTTCTG GTTCCATGGC TGGAGCAACT GCACAGACTT
1051 TTATATATCC AATGGAGGTT ATGAAAACCA GGCTGGCTGT AGGCAAAACT
1101 GGGCAGTACT CTGGAATATA TGATTGTGCC AAGAAGATTT TGAAACATGA
1151 AGGCTTGGGA GCTTTTACA AAGGCTATGT TCCCAATTTA TTAGGTATCA
1201 TACCTTATGC AGGCATAGAT CTTGCTGTGT ATGAGCTCTT GAAGTCCTAT
1251 TGGCTGGATA ATTTTGCAA AGATTCTGTA AACCTGGAG TCATGGTGTT
1301 GCTGGGATGC GGTGCCTTAT CCAGCACCTG TGGTCAGCTG GCCAGCTACC
1351 CATTGGCTTT GGTGAGAACT CGCATGCAGG CTCAAGCCAT GTTAGAAGGT
1401 TCCCCACAGC TGAATATGGT TGGCCTCTTT CGACGAATTA TTTCCAAAGA
1451 AGGAATACCA GGCCTTTACA GAGGCATCAC CCCAAACTTC ATGAAGGTGC
1501 TCCCTGCTGT AGGCATCAGT TATGTGGTTT ATGAAAATAT GAAGCAAAC
1551 TTAGGAGTAA CCCAGAAATG ATGTTGCATT TTTTGCTTTA GCCTGATAAT
1601 TGAAACTTTC AACAATCTCT GGAGTGACTT TTTCTCCTCG AATTGAAACA
1651 AGTCTATGGC AAAAGAAGCT GCATTTTTTT CACAAAAGGG AAGACGGTAA
1701 CAATGGTCAC TTCAAACTTT TGGGCTAAAT TATATGTACA CAGAAATGTT
1751 CAAAATCATA GTTTTAATGT GTTTTGAAAA GGCCACACAA TTATACTTTA
1801 TCTTTTCTTA ATAATCCTGC AAATCTCTGC CCTGAATCCG AAATCTGAAA
1851 ATGTA CTGGC TTGAACAAA TTTGTTTTGT GTGTTAGAGT TATAAATCAT
1901 TAATCTTTAT TTCGGGTGGT TTACGTTTAT GCCAGTTCCT TTATATTTAA
1951 ATTTCTTGTT TTATATATTT TGAATGTCTT TATAGATTTT TTTAAATTTT
2001 CTTATAGAAC CATTAAATAG AAATCATTAC ATTTAAAAATA TACCTTACAG
2051 CAAAAGCATC CAAATAAGTA TAGGGTTTAT GTCCTTATTT TTCTTTCAGC
2101 TGAATACGAA TGAACACAGT GGTGGAATTT CTGAAGGGAA GTGATGAAAT
2151 TATATTTATT TCAGTGGGCA CTTTTCCATT TTACCACTGT ACCATTATTT
2201 GGTTCCTGGA GTTATACACT AATTTTCAGT ATATTACTGT TAAATTACCA
2251 ACACAAGGCA ATTTATTTGA AAGATTCCGT TTATCCTGCC ATTGCTTTGA
2301 AAAGCAGCAG GAAACGAAAT TTTTGTACTT GTATCAGCTT CTGCAGAGCA
2351 TCTTTGTTTT CTTTGTCTT TTTTTCCTA CTTTGTGAAT CAGATTCCGT
2401 TTTAGTCAGG AAGACTTCTT GGGACCATTC TTAGTAACCT GAAATTTCTT
2451 TTTTAATTGC ATGAAGTGGA TTGATCATGA GCAAGTGATG GGCTTTATTT
2501 CTCCCTCACT GGTGAATATC CTTTGAACCT GCTGTTTGCA ATATGGGCAG
2551 CCACAAAGGG GGAGAGATGC CTATTAAATC GGCGGGGTGT ATGACTTCTG
2601 AAAACATTGG ATACCCTATT TTGAAAAGGG AAAGGCCCAA TTTGGGGAAA
2651 CATATACCAA TGCATGATTT CTG (SEQ ID NO:1)

```

FIGURE 1A

FEATURES:

5'UTR: 1-137
Start Codon: 138
Stop Codon: 1569
3'UTR: 1572

HOMOLOGOUS PROTEINS:

Top BLAST Hits:

	Score	E
CRA 335001098641184 /altid=gi 11360341 /def=pir T50686 peroxis...	927	0.0
CRA 11000479457833 /altid=gi 6841066 /def=gb AAF28888.1 AF12330...	834	0.0
CRA 18000005183605 /altid=gi 7504235 /def=pir T22688 hypotheti...	432	e-120
CRA 1000682325160 /altid=gi 7499323 /def=pir T21074 hypothetic...	377	e-103
CRA 89000000196990 /altid=gi 7294582 /def=gb AAF49922.1 (AE003...	348	9e-95
CRA 150000075553401 /altid=gi 9758252 /def=dbj BAB08751.1 (AB0...	339	5e-92
CRA 335001098657884 /altid=gi 11358611 /def=pir T49871 peroxis...	330	2e-89
CRA 163000046661776 /altid=gi 10176874 /def=dbj BAB10081.1 (AB...	326	4e-88
CRA 105000014652720 /altid=gi 10798831 /def=dbj BAB16462.1 (AP...	200	3e-50
CRA 335001098655048 /altid=gi 11277065 /def=pir T47703 Ca-depe...	199	6e-50

BLAST dbEST hits:

gi 10145202 /dataset=dbest /taxon=96...	1108	0.0
gi 1437155 /dataset=dbest /taxon=9606 ...	801	0.0
gi 10333851 /dataset=dbest /taxon=96...	745	0.0
gi 8469752 /dataset=dbest /taxon=960...	363	8e-98
gi 11684041 /dataset=dbest /taxon=96...	307	4e-81

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hits:

gi|10145202 Placenta Choriocarcinoma
gi|1437155 Retina
gi|10333851 Uterus leiomyosarcoma
gi|8469752 Breast
gi|11684041 Ovary fibrotheoma

Expression information from PCR-based tissue screening panels:

Leukocyte

FIGURE 1B

1 MLRWLRDFAL PTAACQDAEQ PTRYETLFQA LDRNGDGWVD IGELQEGLRN
51 LGIPLGQDAE EKIFTTGDVN KDGKLDFFEF MKYLDKHEKK MKLAFKSLDK
101 NNDGKIEASE IVQSLQTLGL TISEQQAELI LQSIDVDGTM TVDWNWRDY
151 FLFNPVTDIE EIIRFWKHST GIDIGDSLTI PDEFTEDKK SGQMMRQLLA
201 GGIAGAVSRT STAPLDRDKI MMQVHGSKSD KMNIFGGFRQ MVKEGGIRSL
251 WRNGNTNVIK IAPETAVKFW AYEYKLLT EEGQKIGTFE RFISGSMAGA
301 TAQTFIYPME VMKTRLAVGK TGQYSGIYDC AKKILKHEGL GAFYKGYVPN
351 LLGIIPYAGI DLAVYELLKS YWLDNFAKDS VNPGMVLLG CGALSSTCGQ
401 LASYPLALVR TRMQAQAMLE GSPQLNMVGL FRRIISKEGI PGLYRGITPN
451 FMKVLPAVGI SYVVYENMKQ TLGVTQK (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

254-257 NGTN (SEQ ID NO:7)

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 2

- 1 229-231 SDK
- 2 475-477 TQK

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 8

- 1 22-25 TRYE (SEQ ID NO:8)
- 2 65-68 TTGD (SEQ ID NO:9)
- 3 121-124 TISE (SEQ ID NO:10)
- 4 157-160 TDIE (SEQ ID NO:11)
- 5 170-173 TGID (SEQ ID NO:12)
- 6 179-182 TIPD (SEQ ID NO:13)
- 7 185-188 TEDE (SEQ ID NO:14)
- 8 227-230 SKSD (SEQ ID NO:15)

[4] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 16

- 1 52-57 GIPLGQ (SEQ ID NO:16)
- 2 119-124 GLTISE (SEQ ID NO:17)
- 3 171-176 GIDIGD (SEQ ID NO:18)
- 4 201-206 GGIAGA (SEQ ID NO:19)
- 5 202-207 GIAGAV (SEQ ID NO:20)
- 6 245-250 GGIRSL (SEQ ID NO:21)
- 7 253-258 GNGTNV (SEQ ID NO:22)
- 8 283-288 GQKIGT (SEQ ID NO:23)
- 9 295-300 GSMAGA (SEQ ID NO:24)
- 10 322-327 GQYSGI (SEQ ID NO:25)
- 11 326-331 GIYDCA (SEQ ID NO:26)
- 12 359-364 GIDLAV (SEQ ID NO:27)
- 13 392-397 GALSST (SEQ ID NO:28)
- 14 399-404 GQLASY (SEQ ID NO:29)

FIGURE 2A

15 442-447 GLYRGI (SEQ ID NO:30)
16 446-451 GITPNF (SEQ ID NO:31)

[5] PDOC00018 PS00018 EF_HAND
EF-hand calcium-binding domain

Number of matches: 3

1 32-44 DRNGDGWVDIGEL (SEQ ID NO:32)
2 68-80 DVNKDGKLDFFEF (SEQ ID NO:33)
3 99-111 DKNNDGKIEASEI (SEQ ID NO:34)

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	292	312	1.053	Certain
2	345	365	0.613	Putative
3	381	401	1.544	Certain
4	446	466	0.733	Putative

BLAST Alignment to Top Hit:

>CRA|335001098641184 /altid=gi|11360341 /def=pir||T50686 peroxisomal
Ca-dependent solute carrier [imported] - rabbit
/org=rabbit /taxon=9986 /dataset=nraa /length=475
Length = 475

Score = 927 bits (2371), Expect = 0.0

Identities = 454/477 (95%), Positives = 466/477 (97%), Gaps = 2/477 (0%)

Query: 1 MLRWLRDFALPTAACQDAEQPTRYETLFQALDRNGDGWVDIGELQEGLRNGLGIPLGQDAE 60
MLRWLR F LPTAACQ AE PTRYETLFQALDRNGDGWVDI ELQEGL++LGIPLGQDAE
Sbjct: 1 MLRWLRGFVLPTAACQGAEPTRYETLFQALDRNGDGWDIRELQEGLKSLGIPLGQDAE 60

Query: 61 EKIFTTGDVKNKGKLDFFEFMKYLLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL 120
EKIFTTGDVKNKGKLDFFEFMKYLLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL
Sbjct: 61 EKIFTTGDVKNKGKLDFFEFMKYLLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL 120

Query: 121 TISEQQAELILQSIDVGTMTVDWNEWRDYFLFNPVTDIEEIRFWKHSTGIDIGDSLTI 180
TISEQQAELILQSID DGTMTVDWNEWRDYFLFNPV DIEEIRFWKHSTGIDIGDSLTI
Sbjct: 121 TISEQQAELILQSIDADGTMTVDWNEWRDYFLFNPVADIEEIRFWKHSTGIDIGDSLTI 180

Query: 181 PDEFTEDEKKSQGWWRQLLAGGIAGAVSRTSTAPLDRLLKIMQVHGSKSDKMNIFFGGFRQ 240
PDEFTE+E+KSGQWWRQLLAGGIAGAVSRTSTAPLDRLLK+HMQVHGSKS MNIFFGGFRQ
Sbjct: 181 PDEFTEERKSQGWWRQLLAGGIAGAVSRTSTAPLDRLLKVMQVHGSKS--MNIFFGGFRQ 238

Query: 241 MVKEGGIRSLWRGNGTNVIKIPETAVKFWAYEQYKLLTEEGQKIGTFERFISGSMAGA 300
M+KEGG+RSLWRGNGTNVIKIPETAVKFW YEYKLLTEEGQKIGTFERFISGSMAGA
Sbjct: 239 MIKEGGVRSLWRGNGTNVIKIPETAVKFWVYEQYKLLTEEGQKIGTFERFISGSMAGA 298

Query: 301 TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGI 360
TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILK+EG GAFYKGYVPNLLGIIPYAGI
Sbjct: 299 TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKYEGFGAFYKGYVPNLLGIIPYAGI 358

Query: 361 DLAVYELLKSYWLDNFAKDSVNPVGMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE 420
DLAVYELLKS+WLDNFAKDSVNPVGM+VLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE
Sbjct: 359 DLAVYELLKSHWLDNFAKDSVNPVGLVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE 418

FIGURE 2B

Query: 421 GSPQLNMVGLFRRISKEGIPGLYRGITPNFMKVLPAVGISYVYENMKQTLGVTQK 477 (residues 1-477 of SEQ ID NO:2)

G+PQLNMVGLFRRISKEG+PGLYRGITPNFMKVLPAVGISYVYENMKQTLGVTQK

Sbjct: 419 GAPQLNMVGLFRRISKEGLPGLYRGITPNFMKVLPAVGISYVYENMKQTLGVTQK 475
(SEQ ID NO:4)

>CRA|11000479457833 /altid=gi|6841066 /def=gb|AAF28888.1|AF123303_1
(AF123303) calcium-binding transporter [Homo sapiens]
/org=Homo sapiens /taxon=9606 /dataset=nraa /length=411
Length = 411

Score = 834 bits (2132), Expect = 0.0
Identities = 409/410 (99%), Positives = 409/410 (99%)

Query: 8 FALPTAACQDAEQPTRYETLFOALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTG 67

F LPTAACQDAEQPTRYETLFOALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTG
Sbjct: 1 FVLPTAACQDAEQPTRYETLFOALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTG 60

Query: 68 DVNKGKLDFFEEMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQA 127

DVNKGKLDFFEEMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQA
Sbjct: 61 DVNKGKLDFFEEMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQA 120

Query: 128 ELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIIRFWKHSTGIDIGDSLTPDEFTD 187

ELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIIRFWKHSTGIDIGDSLTPDEFTD
Sbjct: 121 ELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIIRFWKHSTGIDIGDSLTPDEFTD 180

Query: 188 EKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMVHGSKSDKMNIFFGGFRQMVKEGGI 247

EKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMVHGSKSDKMNIFFGGFRQMVKEGGI
Sbjct: 181 EKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMVHGSKSDKMNIFFGGFRQMVKEGGI 240

Query: 248 RSLWRGNGTNVIKIAPETAVKFWAYEQYKLLTTEGQKIGTFERFISGSMAGATAQTFIY 307

RSLWRGNGTNVIKIAPETAVKFWAYEQYKLLTTEGQKIGTFERFISGSMAGATAQTFIY
Sbjct: 241 RSLWRGNGTNVIKIAPETAVKFWAYEQYKLLTTEGQKIGTFERFISGSMAGATAQTFIY 300

Query: 308 PMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYEL 367

PMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYEL
Sbjct: 301 PMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYEL 360

Query: 368 LKSYWLDNFAKDSVNPVGMVLLGCGALSSTCGQLASYPLALVRTRMQAQA 417 (residues 8-417 of
SEQ ID NO:2)

LKSYWLDNFAKDSVNPVGMVLLGCGALSSTCGQLASYPLALVRTRMQAQA

Sbjct: 361 LKSYWLDNFAKDSVNPVGMVLLGCGALSSTCGQLASYPLALVRTRMQAQA 410
(SEQ ID NO:5)

Score = 80.0 bits (194), Expect = 6e-14
Identities = 80/388 (20%), Positives = 156/388 (39%), Gaps = 59/388 (15%)

Query: 95 FKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDV--DGTMTVDWNEWRDYFL 152

F++LD+N DG ++ E+ + L+ LG+ ++ E I + DV DG +
Sbjct: 21 FQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTGDNVKGKLD----- 68

Query: 153 FNPVTDIEEIIIRFWKHSTGIDIGDSLTPDEFTDEKKSGQWWRQLLAGGIAGAVSRTST 212

D EE +++ K + EKK ++ L +
Sbjct: 69 -----DFFEEMKYLK-----DHEKKMKLAFKSLDKNNDGKIEASEIV 105

Query: 213 APLDRLKIMMVHGSKSDKMNIFFGGFRQMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAY 272

L L ++ ++ +I V R + N I E ++FW +
Sbjct: 106 QSLQTLGLTISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDI----EEIIRFWKH 161

FIGURE 2C

Query: 273 EQYKKL-----LTEEGQKIGTFER-FISGSMAGATAQTFIYPMEVMKTRLAV-GKT 321
+ TE+ +K G + R ++G +AGA ++T P++ +K + V G
Sbjct: 162 STGIDIGDSLTIPTDEFTDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSK 221

Query: 322 GQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLDNFAKDSV 381
I+ +++K G+ + ++G N++ I P + YE K ++
Sbjct: 222 SDKMNIFGGFRQMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKL-----LTEEGQ 277

Query: 382 NPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQLNMVGLFRRIISKEGIP 441
G G+++ Q YP+ +++TR+ A+ + + ++I+ EG+
Sbjct: 278 KIGTFERFISGSMAGATAQTFIYPMEVMKTRL---AVGKTGQYSGIYDCAKKILKHEGLG 334

Query: 442 GLYRGITPNFMKVLPAVGISYVYENMK 469 (residues 95-469 of SEQ ID NO:2)
Y+G PN + ++P GI VYE +K
Sbjct: 335 AFYKGYVPNLLGIIPYAGIDLAVYELLK 362 (SEQ ID NO:6)

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00153	Mitochondrial carrier proteins	305.4	3e-88	1
PF00036	EF hand	50.7	1.7e-12	3
PF00404	Dockerin domain type I	9.7	0.26	1
PF01978	Protein of unknown function	2.7	9.5	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00036	1/3	27	51 ..	5	29 .]	18.7	0.002
PF00404	1/1	67	85 ..	1	22 []	9.7	0.26
PF00036	2/3	61	87 ..	3	29 .]	19.7	0.001
PF00036	3/3	90	118 ..	1	29 []	17.2	0.0051
PF01978	1/1	110	121 ..	1	13 [.]	2.7	9.5
PF00153	1/1	193	472 ..	1	313 []	305.4	3e-88

FIGURE 2D